Au 1812

Page: 1 Raw Sequence Listing

74/2 04/12/93 13:26:14 04/1/93 S4317.ray

1 2 3		sequence listing
4 5	(1) GENE	RAL INFORMATION:
6 7 8	(i)	APPLICANT: Israel, David Wolfman, Neil M
9 10	(ii)	TITLE OF INVENTION: RECOMBINANT BONE MORPHOGENETIC PROTEIN HETERODIMERS, COMPOSITIONS AND METHODS OF USE
11 12 13	(iii)	NUMBER OF SEQUENCES: 35
14 15 16 17 18 19	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc. (B) STREET: 87 CambridgePark Drive (C) CITY: Cambridge (D) STATE: MA (E) COUNTRY: USA (F) ZIP: 02140-2387
21 22 23 24 25 26 27	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28 29 30 31 32	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US 07/864,692 (B) FILING DATE: 07-APR-1992 (C) CLASSIFICATION:
33 34 35 36 37	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Kapinos, Ellen J. (B) REGISTRATION NUMBER: 32,245 (C) REFERENCE/DOCKET NUMBER: GI-5192A
38 39 40 41 42	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 617 876-1170 (B) TELEFAX: 617 876-5851
43 44	(2) INFO	RMATION FOR SEQ ID NO:1:
45 46 47 48 49 50		SEQUENCE CHARACTERISTICS: (A) LENGTH: 1607 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown
51 52	(11)	MOLECULE TYPE: DNA

Raw Sequence Listing

04/12/93 13:26:15 S4317.raw

53 54 55		(ix)		ATURI A) NI		ZEV.	CDG										
56				B) L(•			154	13								
57																	
58																	
59 60		(xi)) SE	QUEN	CE DI	ESCR:	[PTI	ON: S	SEQ :	ID NO	0:1:						
61	GTC	GACT	CTA (GAGT	GTGT(T C	AGCA	CTTG	G CT	GGGG2	ACTT	CTT	GAAC'	rTG ·	CAGG	AGAAT	60
62 63	AAC'	rtgc	GCA (cccc	ACTT'	rg co	3CCG(STGC	c TT:	rgcc	CCAG	CGG	AGCCT	rgc '	TTCGO	CATCT	120
64																	
65 66	CCG	AGCC	CCA (CCGC	CCT	CC A	CTCC:	rcgg	CT	rgcc	CGAC	ACT	GAGA	CGC '	TGTT	CCAGC	180
67	GTG	AAAA	GAG 2	AGACI	rgcgo	CG G	CCGG	CACC	G GGG	GAGA	AGGA	GGA	GCA	AAG .	AAAA	GAACG	240
68	~- ~																
69 70	GAC	ATTC	GT (CCTT	3CGC(CA GO	FTCC:	rttg2	A CC2	AGAG'	rttt	TCC	ATGT	3GA	CGCT	CTTTCA	300
71	ATG	JACG:	rgt (cccc	CGT	GC T	rctt2	AGAC	GA(CTGC	GTC	TCC	CAAA1	GT	CGAC	ATG	358
72 73																Met	
73 74																1	
75	GTG	GCC	GGG	ACC	CGC	TGT	CTT	CTA	GCG	TTG	CTG	CTT	CCC	CAG	GTC	CTC	406
76	Val	Ala	Gly	Thr	Arg	Сув	Leu	Leu	Ala	Leu	Leu	Leu	Pro	Gln	Val	Leu	
77				5					10					15			
78	ama	000	000	000	aam	000	ama	omm.	aaa	~~	ama	aaa	999			mma	454
79 80															AAG Lys		454
81		OL,	20	7114	71_4	017		25		014	200	01	30	y	2,5	1110	
82																	
83															GAG		502
84	Ala		Ala	Ser	Ser	Gly		Pro	Ser	Ser	Gln		Ser	Asp	Glu	Val	
85 86		35					40					45					
87	CTG	AGC	GAG	TTC	GAG	TTG	CGG	CTG	CTC	AGC	ATG	TTC	GGC	CTG	AAA	CAG	550
88	Leu	Ser	Glu	Phe	Glu	Leu	Arg	Leu	Leu	Ser	Met	Phe	Gly	Leu	Lys	Gln	
89	50					55					60					65	
90							a. a	999	ama	ama		~~~			am.	a. a	500
91 92															CTA Leu		598
93	9				70	9	nop.	****	141	75		110	-1-	MCC	80	MDP	
94																	
95															GAC		646
96	Leu	Tyr	Arg	_	His	Ser	Gly	Gln		Gly	Ser	Pro	Ala		Asp	His	
97 98				85					90					95			
99	CGG	TTG	GAG	AGG	GCA	GCC	AGC	CGA	GCC	AAC	ACT	GTG	CGC	AGC	TTC	CAC	694
100															Phe		
101	_		100	_				105					110				
102																	
103															ACA		742
104	nls	GIU	GIU	ser	neu	GIU	GIU	neu	PIO	GIU	Inr	ser	стА	гЛя	Thr	III	

Raw Sequence Listing

04/12/93 13:26:16 S4317.raw

105 106		115					120					125					
107	CGG	AGA	TTC	TTC	ттт	AAT	тта	AGT	тст	ΑΤС	מממ	ACG.	GAG	GAG	ттт	איזיכי	790
108		Arg															,50
109	130	3				135					140			0_0		145	
110																	
111	ACC	TCA	GCA	GAG	СТТ	CAG	GTT	TTC	CGA	GAA	CAG	АТС	CAA	САТ	GCT	тта	838
112		Ser															030
113					150				5	155			·		160		
114																	
115	GGA	AAC	AAT	AGC	AGT	TTC	CAT	CAC	CGA	ATT	аат	ATT	TAT	GAA	ATC	АТА	886
116		Asn															
117	4			165					170				-1-	175			
118																	
119	AAA	CCT	GCA	ACA	GCC	AAC	TCG	AAA	TTC	CCC	GTG	ACC	AGA	CTT	TTG	GAC	934
120		Pro															
121	•		180					185					190				
122																	
123	ACC	AGG	TTG	GTG	AAT	CAG	AAT	GCA	AGC	AGG	TGG	GAA	ACT	TTT	GAT	GTC	982
124	Thr	Arg	Leu	Val	Asn	Gln	Asn	Ala	Ser	Arg	Trp	Glu	Thr	Phe	Asp	Val	
125		195					200			_	_	205			_		
126																	
127	ACC	CCC	GCT	GTG	ATG	CGG	TGG	ACT	GCA	CAG	GGA	CAC	GCC	AAC	CAT	GGA	1030
128	Thr	Pro	Ala	Val	Met	Arg	Trp	Thr	Ala	${\tt Gln}$	Gly	His	Ala	Asn	His	Gly	
129	210					215					220					225	
130																	
131	TTC	GTG	GTG	GAA	GTG	GCC	CAC	TTG	GAG	GAG	AAA	CAA	GGT	GTC	TCC	AAG	1078
132	Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	Lys	${\tt Gln}$	Gly	Val	Ser	Lys	
133					230					235					240		
134																	
135		CAT															1126
136	Arg	His	Val		Ile	Ser	Arg	Ser		His	Gln	Asp	Glu		Ser	\mathtt{Trp}	
137				245					250					255			
138																	
139		CAG															1174
140	Ser	Gln		Arg	Pro	Leu	Leu		Thr	Phe	GIĀ	His		СТĀ	Lys	GTA	
141			260					265					270				
142 143	CAT	CCT	ama	as a	***	202	C13.3	***	CCT	C2 2	aaa	***	as a	***	CAC	CCC	1222
		Pro															1222
144 145	UIS	275	пеп	UTD	пур	ALG	280	цув	Arg	GIII	ALG	285	пто	пув	GIII	Arg	
146		2/3					200					203					
147	222	CGC	Curur	AAG	דרר	ACC	тст	AAG	ACA	CAC	רכיזי	ጥጥር	ጥ ል ር	GTG.	GAC	ጥጥር	1270
148		Arg															1270
149	290	9		_,_	501	295	0,0	-70	9		300		-1-	,		305	
150						_,,										-	
151	AGT	GAC	GTG	GGG	TGG	AAT	GAC	TGG	ATT	GTG	GCT	CCC	CCG	GGG	TAT	CAC	1318
152		Asp															-
153				4	310					315					320		
154																	
155	GCC	TTT	TAC	TGC	CAC	GGA	GAA	TGC	CCT	TTT	CCT	CTG	GCT	GAT	CAT	CTG	1366
156	Ala	Phe	Tyr	Сув	His	Gly	Glu	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	

Raw Sequence Listing

04/12/93 13:26:17 S4317.raw

157				325					330					335			
158		maa	. cm		~	~~~		~~~	~~ ~			~~~			~		7.47.4
159 160				AAT Asn													1414
161	Abii	261	340	Abii	птв	AIG	116	345	GIII	1111	пеп	val	350	Ser	vai	ABII	
162			3.0					313					330				
163	TCT	AAG	ATT	CCT	AAG	GCA	TGC	TGT	GTC	CCG	ACA	GAA	CTC	AGT	GCT	ATC	1462
164				Pro													-
165		355			_		360	_				365					
166																	
167				TAC													1510
168		Met	Leu	Tyr	Leu		Glu	Asn	Glu	Lys		Val	Leu	Lys	Asn		
169	370					375					380					385	
170																	
171												TAG:	raca(GCA A	AAAT'	TAAAT	A 1563
172 173	GIN	Asp	Met	Val		GIU	GTĀ	Сув	GIĀ		Arg						
1/3 174					390					395							
175	СУП	ידיגגי	י גידיג	TATA:	ימידימי	יים מיו	ייי אייי	ריייי א נ	י א א		מממי	***	۸.				1607
176	CAI	WWI	MIM .	IAIA.	LAIA.	IW I	TAT.	LIIA	3 MAI	MMM	JAAA	MMM	•				1607
177																	
178	(2)	INF	ORMA'	TION	FOR	SEO	ID i	NO: 2	:								
179	(-,								*								
180			(i)	SEQUI	ENCE	CHAI	RACTI	RIS'	rics:	:							
181				(A)	LEI	NGTH	: 396	am:	ino a	acida	s						
182				(B)	TY	PE: a	amino	ac:	id								
183						POLO											
184																	
184 185		(:	ii) 1		TO	POLO	3Y:]	linea	ar								
184 185 186				(D)	TO	POLO(3Y:] 3: p:	linea rote:	ar in								
184 185 186 187				(D)	TO	POLO(3Y:] 3: p:	linea rote:	ar in	Q ID	NO:2	2:					
184 185 186 187 188	15-4	(:	xi) :	(D) MOLE(SEQUI	TOICULE	POLO TYPI DES	SY:] S: p: CRIP!	linea rote: rion	ar in : SE(•			T	P	GI-	17-1	
184 185 186 187 188 189		(:	xi) :	(D)	TOICULE SNCE	POLO TYPI DES	SY:] S: p: CRIP!	linea rote: rion	ar in : SE(Ala			Leu	Pro		Val	
184 185 186 187 188 189	Met 1	(:	xi) :	(D) MOLE(SEQUI	TOICULE	POLO TYPI DES	SY:] S: p: CRIP!	linea rote: rion	ar in : SE(•			Leu	Pro	Gln 15	Val	
184 185 186 187 188 189 190	1	(: Val	xi) :	(D) MOLEC SEQUE	TOI CULE ENCE Thr	TYPI DESC Arg	GY:] G: pi CRIPT Cys	linea rote: rion Leu	ar in : SE(Ala 10	Leu	Leu			15		
184 185 186 187 188 189 190 191	1	(: Val	xi) :	(D) MOLE(SEQUI Gly	TOI CULE ENCE Thr	TYPI DESC Arg	GY:] G: pi CRIPT Cys	linea rote: rion Leu	ar in : SE(Leu Val	Ala 10	Leu	Leu		Arg	15		
184 185 186 187 188 189 190	1	(: Val	xi) :	(D) MOLEC SEQUE	TOI CULE ENCE Thr	TYPI DESC Arg	GY:] G: pi CRIPT Cys	linea rote: rion Leu	ar in : SE(Ala 10	Leu	Leu			15		
184 185 186 187 188 189 190 191 192	1 Leu	(z Val Leu	xi) { Ala Gly	(D) MOLE(SEQUI Gly	TOLE ENCE Thr 5	TYPI DESC Arg	GY:] CRIPT Cys Gly	linea rote: rion Leu Leu	in : SEÇ Leu Val 25	Ala 10 Pro	Leu Glu	Leu Leu	Gly	Arg 30	15 Arg	Lys	
184 185 186 187 188 189 190 191 192 193 194	1 Leu	(z Val Leu	xi) { Ala Gly	(D) MOLEG SEQUE Gly Gly 20	TOLE ENCE Thr 5	TYPI DESC Arg	GY:] CRIPT Cys Gly	linea rote: rion Leu Leu	in : SEÇ Leu Val 25	Ala 10 Pro	Leu Glu	Leu Leu	Gly	Arg 30	15 Arg	Lys	
184 185 186 187 188 189 190 191 192 193 194 195 196	1 Leu Phe	Val Leu Ala	Ala Gly Ala 35	(D) MOLEG SEQUE Gly Gly 20 Ala	CULE SNCE Thr 5 Ala	TYPI DESC Arg Ala Ser	GY: I	lines rote: rION Leu Leu Arg 40	in : SEG Leu Val 25	Ala 10 Pro	Leu Glu Ser	Leu Leu Gln	Gly Pro 45	Arg 30 Ser	15 Arg Asp	Lys Glu	
184 185 186 187 188 189 190 191 192 193 194 195 196 197	1 Leu Phe	Val Leu Ala	Ala Gly Ala 35	(D) MOLEG SEQUE Gly Gly 20	CULE SNCE Thr 5 Ala	TYPI DESC Arg Ala Ser	GY: I GRIPT Cys Gly Gly Leu	lines rote: rION Leu Leu Arg 40	in : SEG Leu Val 25	Ala 10 Pro	Leu Glu Ser	Leu Leu Gln Met	Gly Pro 45	Arg 30 Ser	15 Arg Asp	Lys Glu	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198	1 Leu Phe	Val Leu Ala	Ala Gly Ala 35	(D) MOLEG SEQUE Gly Gly 20 Ala	CULE SNCE Thr 5 Ala	TYPI DESC Arg Ala Ser	GY: I	lines rote: rION Leu Leu Arg 40	in : SEG Leu Val 25	Ala 10 Pro	Leu Glu Ser	Leu Leu Gln	Gly Pro 45	Arg 30 Ser	15 Arg Asp	Lys Glu	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	1 Leu Phe Val	Val Leu Ala Leu 50	Ala Gly Ala 35 Ser	(D) MOLEG SEQUI Gly 20 Ala Glu	TOI CULE ENCE Thr 5 Ala Ser	TYPI DESC Arg Ala Ser	GY: 1 CRIPT Cys Gly Gly Leu 55	rote: FION Leu Leu Arg 40	in ESEÇ Leu Val 25 Pro Leu	Ala 10 Pro Ser	Leu Glu Ser	Leu Gln Met 60	Gly Pro 45	Arg 30 Ser Gly	15 Arg Asp Leu	Lys Glu Lys	
184 185 186 187 188 190 191 192 193 194 195 196 197 198 199 200 201	Leu Phe Val	Val Leu Ala Leu 50	Ala Gly Ala 35 Ser	(D) MOLEG SEQUE Gly Gly 20 Ala	TOI CULE ENCE Thr 5 Ala Ser	TYPI DESC Arg Ala Ser Glu Ser	GY: 1 CRIPT Cys Gly Gly Leu 55	rote: FION Leu Leu Arg 40	in ESEÇ Leu Val 25 Pro Leu	Ala 10 Pro Ser	Leu Glu Ser Ser	Leu Gln Met 60	Gly Pro 45	Arg 30 Ser Gly	15 Arg Asp Leu	Lys Glu Lys Leu	
184 185 186 187 188 190 191 192 193 194 195 196 197 198 199 200 201 202	1 Leu Phe Val	Val Leu Ala Leu 50	Ala Gly Ala 35 Ser	(D) MOLEG SEQUI Gly 20 Ala Glu	TOI CULE ENCE Thr 5 Ala Ser	TYPI DESC Arg Ala Ser	GY: 1 CRIPT Cys Gly Gly Leu 55	rote: FION Leu Leu Arg 40	in ESEÇ Leu Val 25 Pro Leu	Ala 10 Pro Ser	Leu Glu Ser	Leu Gln Met 60	Gly Pro 45	Arg 30 Ser Gly	15 Arg Asp Leu	Lys Glu Lys	
184 185 186 187 188 190 191 192 193 194 195 196 197 198 199 200 201 202 203	Leu Phe Val Gln 65	Val Leu Ala Leu 50 Arg	Ala Gly Ala 35 Ser	(D) MOLE(SEQUE Gly 20 Ala Glu Thr	TOI CULE ENCE Thr 5 Ala Ser Phe	POLOG TYPI DESG Arg Ala Ser Glu Ser 70	GY: I E: pr CRIPT Cys Gly Gly Leu 55	Lines FION Leu Leu Arg 40 Arg	in ESEÇ Leu Val 25 Pro Leu Ala	Ala 10 Pro Ser Leu Val	Leu Glu Ser Ser Val	Leu Gln Met 60	Gly Pro 45 Phe	Arg 30 Ser Gly	15 Arg Asp Leu Met	Lys Glu Lys Leu 80	
184 185 186 187 188 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204	Leu Phe Val Gln 65	Val Leu Ala Leu 50 Arg	Ala Gly Ala 35 Ser	(D) MOLEG SEQUI Gly 20 Ala Glu	TOI CULE ENCE Thr 5 Ala Ser Phe Pro	POLOG TYPI DESG Arg Ala Ser Glu Ser 70	GY: I E: pr CRIPT Cys Gly Gly Leu 55	Lines FION Leu Leu Arg 40 Arg	in ESEÇ Leu Val 25 Pro Leu Ala	Ala 10 Pro Ser Leu Val	Leu Glu Ser Ser Val	Leu Gln Met 60	Gly Pro 45 Phe	Arg 30 Ser Gly	15 Arg Asp Leu Met	Lys Glu Lys Leu 80	
184 185 186 187 188 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205	Leu Phe Val Gln 65	Val Leu Ala Leu 50 Arg	Ala Gly Ala 35 Ser	(D) MOLE(SEQUE Gly 20 Ala Glu Thr	TOI CULE ENCE Thr 5 Ala Ser Phe	POLOG TYPI DESG Arg Ala Ser Glu Ser 70	GY: I E: pr CRIPT Cys Gly Gly Leu 55	Lines FION Leu Leu Arg 40 Arg	in ESEÇ Leu Val 25 Pro Leu Ala	Ala 10 Pro Ser Leu Val	Leu Glu Ser Ser Val	Leu Gln Met 60	Gly Pro 45 Phe	Arg 30 Ser Gly	15 Arg Asp Leu Met	Lys Glu Lys Leu 80	
184 185 186 187 188 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206	Leu Phe Val Gln 65 Asp	Val Leu Ala Leu 50 Arg	Ala Gly Ala 35 Ser Pro	(D) MOLE(SEQUE Gly 20 Ala Glu Thr	TOI CULE ENCE Thr 5 Ala Ser Phe Pro	POLOG TYPI DESC Arg Ala Ser Glu Ser 70	GY: I G: pr CRIPT Cys Gly Gly Leu 55 Arg	Lines FION Leu Leu Arg 40 Arg Asp	in : SEG Leu Val 25 Pro Leu Ala	Ala 10 Pro Ser Leu Val	Leu Glu Ser Ser Val 75	Leu Gln Met 60 Pro	Gly Pro 45 Phe Pro	Arg 30 Ser Gly Tyr	Asp Leu Met	Lys Glu Lys Leu 80 Asp	
184 185 186 187 188 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205	Leu Phe Val Gln 65 Asp	Val Leu Ala Leu 50 Arg	Ala Gly Ala 35 Ser Pro	(D) MOLE(SEQUE Gly 20 Ala Glu Thr	TOI CULE ENCE Thr 5 Ala Ser Phe Pro	POLOG TYPI DESC Arg Ala Ser Glu Ser 70	GY: I G: pr CRIPT Cys Gly Gly Leu 55 Arg	Lines FION Leu Leu Arg 40 Arg Asp	in : SEG Leu Val 25 Pro Leu Ala	Ala 10 Pro Ser Leu Val	Leu Glu Ser Ser Val 75	Leu Gln Met 60 Pro	Gly Pro 45 Phe Pro	Arg 30 Ser Gly Tyr	Asp Leu Met	Lys Glu Lys Leu 80 Asp	

Raw Sequence Listing

04/12/93 13:26:18 S4317.raw

209	***	774 -	a 1	~1	a	T	43	a1	•	D	~ 1	m\		~ 1	•	m1
210 211	HIB	HIB	Glu 115	GIU	ser	Leu	GIU		гел	Pro	GIU	Thr		GIY	гля	Thr
211			113					120					125			
212	mb	7	Arg	Dha	Dho	Dho	7	T	Com	C	T1.	D	mb	a1	a 1	Db.
214	1111	130	ALG	FIIG	FIIG	FIIG	135	пеп	ser	ser	TTG	140	IIII	GIU	GIU	Pile
215		130					133					140				
216	Tla	Th.	Ser	λla	G1.,	Lou	Gln.	17n 1	Dho	7-~	G1	Cln.	Wot	Cln	N an	710
217	145	1111	Der	ATG	GIU	150	GIII	Val	FIIG	ALG	155	GIII	Mec	GIII	Авр	160
218	140					130					133					100
219	T 011	C1	7 ~~	7 00	C0=	C.~	Dho	ui a	ui.	N	T1.	3 an	т1.	т	<u>ما</u>	T1.
220	пеа	GIY	Asn	VOII	165	per	FIIG	urs	urs	170	TIE	ABII	TTE	ıyı	175	TTG
221					103					170					1/5	
222	Tla	T.370	Pro	Δla	Thr	Δla	Aan	Sar	Tara	Dha	Dro	Wa I	Thr	λτα	T.A11	T.011
223	110	ду Б	110	180	1111	ALG	AOII	Der	185	1110	210	Val		190	пес	пеа
224				100					100					150		
225	λαη	Thr	Arg	T.011	77a]	Δen	G] n	λen	λla	Ser	Ara	Trn	<i>G</i> 111	Thr	Dhe	Agn
226	nop	****	195	пец	Val	ADII	GIII	200	AIG	261	ALG	115	205	1111	1116	rep
227								200					200			
228	Val	Thr	Pro	Ala	Val	Met	Ara	Tro	Thr	Ala	Gln	Glv	His	Ala	Agn	His
229		210					215					220				
230																
231	Glv	Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	Lvs	Gln	Glv	Val	Ser
232	225					230					235	-2-		1		240
233																
234	Lvs	Ara	His	Val	Arg	Ile	Ser	Arg	Ser	Leu	His	Gln	Asp	Glu	His	Ser
235	•				245					250					255	
236																
237	Trp	Ser	Gln	Ile	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly	His	Asp	Gly	Lys
238				260	_				265			_		270	_	-
239																
240	Gly	His	Pro	Leu	His	Lys	Arg	Glu	Lys	Arg	Gln	Ala	Lys	His	Lys	Gln
241			275					280					285			
242																
243	Arg	Lys	Arg	Leu	Lys	Ser	Ser	Сув	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp
244		290					295					300				
245																
246	Phe	Ser	Asp	Val	Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr
247	305					310					315					320
248																
249	His	Ala	Phe	Tyr	_	His	Gly	Glu	Cys		Phe	Pro	Leu	Ala	Asp	His
250					325					330					335	
251							_	_	_	_	_					_
252	Leu	Asn	Ser		Asn	His	Ala	Ile		Gln	Thr	Leu	Val		Ser	Val
253				340					345					350		
254	_	_	_		_	_		_	_		_		 -	_	_	
255	Asn	Ser	_	Ile	Pro	Lys	Ala	_	Сув	Val	Pro	Thr		Leu	Ser	Ala
256			355					360					365			
257		a .	35. 4	-	_		•	~ 7	•	~ 7		**. *		• .	.	.
258	TTE		Met	ьeu	ıyr	ьeп	_	Glu	Asn	GLu	га		val	Leu	гав	Asn
259		370					375					380				
260																

Raw Sequence Listing

04/12/93 13:26:19 S4317.raw

261 262 263	Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg 385 390 395	
264 265	(2) INFORMATION FOR SEQ ID NO:3:	
266 267 268	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1954 base pairs(B) TYPE: nucleic acid	
269 270		
271 272	(ii) MOLECULE TYPE: DNA	
273 274		
275 276	(ix) FEATURE: (A) NAME/KEY: CDS	
277 278	V==, ======, ==========================	
279 280	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
281 282	CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA	60
283 284	GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG	120
285 286	AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC	180
287 288	ACAGTCCCCG GCCCTCGCCC AGGTTCACTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG	240
289 290	CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC	300
291 292	GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG CTGTCAAGAA	360
293 294	TCATGGACTG TTATTATATG CCTTGTTTTC TGTCAAGACA CC ATG ATT CCT GGT	414
295 296	Met Ile Pro Gly 1	
297 298	· · · · · · · · · · · · · · · · · · ·	462
299 300	Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly 5 10 15 20	
301 302	GCG AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC	510
303 304	Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala 25 30 35	
305 306	GAG ATT CAG GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG	558
307 308	Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu 40 45 50	
309 310	CTC CTG CGG GAC TTC GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC	606
311 312	Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met Phe Gly Leu Arg 55 60 65	

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1314 CGC CCC CCG CAG CCT AGC AAG AAG AGT GCC GTC ATT CCG GAC TAC ATG CGG 654 156 70 316 70 75 157 75 80 158 Asp Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro Asp Tyr Met Arg 159 Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu Glu Glu Glu Glu His His 150 90 95 1000 121 Asp Leu Tyr Arg Leu Gln Ser Gly Glu	313																	
116	314																	654
SAT CTT TAC CGG CTT CAG TCT GGG GAG GAG GAG GAG GAG GAG CAC CAC SAF Lew Tyr Arg Lew Gin Ser Gly Glu Glu Glu Glu Glu Glu Gln 11e His Sag Lew Tyr Arg Lew Gin Ser Gly Glu		Arg		Pro	Gln	Pro	Ser		Ser	Ala	Val	Ile		Asp	Tyr	Met	Arg	
118 SAT CTT TAC CGG CTT CAG TCT GGG GAG GAG GAG GAG GAG GAG CAG ATC CAC 102 103 104 105 104 104 104 105 104 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105 105			70					75					80					
19																		
Second S																		702
321 AGC ACT GGT CTT GAG TAT CCT GAG CCG CCG GCC AGC CAG CAG ACC			Leu	Tyr	Arg	Leu		Ser	Gly	Glu	Glu		Glu	Glu	Gln	Ile		
See Acc Acc Get Ctt Gag Tat Ctt Gag Ccc Ccc Gcc Acc Ccc Acc		85					90					95					100	
See																		
110 115 116 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118 118																		750
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326 STG AGG AGC CAC CAC CAC GAA GAA CAT CTG GAG ACC ATC CAC GGG ACC						102					110					115		
327		~~~			mm.a	~- ~	~- ~											
120		_																798
329 330 AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC CCT S466 S27 S27		vaı	Arg	ser		HIS	HIS	GIU	GIU		ren	GIU	Asn	TTE		GIY	Thr	
331					120					125					130			
Ser Glu Ash Ser Ala Phe Arg Phe Leu Phe Ash Leu Ser Ser Ile Pro 145		a cum	CAA	220	m/m	com	mmm	aam	mma	ama	mmm	330	ama	3.00	3.00	3.00	aam	946
332 333 334 346 347 347 347 347 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348 348																		846
334		Ser	GIU		Ser	ATA	Pne	Arg		теп	Pne	ABII	Leu		ser	тте	Pro	
Same				133					140					143				
336 Silva Ash Glu Val Silva Silva		GNG	3 A C	GNG	CTC	አ ጥር	TCC	ጥርጥ	CCA	CAC	Стт	caa	CTC	ጥጥረ	000	434	CNC	904
150																		034
337 338 GTG GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT 339 Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile 340 165 341 342 TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC 343 Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile 344 185 346 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG 347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp 348 350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 352 215 220 215 220 216 220 220 220 220 220 220 220 220 220 22		Gru		GIU	VAI	116	261		ALG	GIU	пеп	Arg		FIIG	Arg	GIU	GIII	
338			130					133					100					
339		стс	GAC	CAG	ממכ	ССТ	СУТ	тсс	GAA	» GG	GGC	ጥጥር	CAC	ССТ	מידמ	220	ידידי מ	942
340 165 170 175 180 341 342 TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC 990 343 Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile 185 185 190 195 344 185 CTG GTC CAC CAC AAT GTG ACA CGG TGG 195 195 195 345 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG 1038 195 195 347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp 210 205 205 210 349 200 E CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG 1086 1086 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 225 225 352 215 220 220 225 353 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 1134 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Gln Thr 240 235 357 235 240 357 240 358 CGG ACC CAC CAC GAG GGC CAG CAT GTC AGG ATT AGC CTA TAG CT CAA 1182 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 255 361 245 250																		742
341 342 TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC 343 Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile 344 185			rob	G111	GLY	210	_	TTP	GIU	nr 9	Gry		HID	ALG	116	ABII		
342 TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC 990 343 Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile 195 344 185 Pro Pro Ala Glu Val Val Pro Gly His Leu Ile 195 345 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG 1038 346 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG 1038 347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp 210 210 348 200 Fro AGC CTC GCG GTC CTC CGC GTG ACC CGG GAG AAG 1086 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 225 352 215 Fro Aga CTC ATT GAG GTG ACT CAC CTC CAT CAG ACT CAG ACT 1134 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT CAG ACT CAG ACT CAG ACT CAG							-,0					1,3					100	
343 Tyr Glu Val Met Lys Pro Pro Ala Glu Val Pro Gly His Leu Ile 344 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 <td></td> <td>ТАТ</td> <td>GAG</td> <td>GTT</td> <td>ATG</td> <td>AAG</td> <td>מממ</td> <td>CCA</td> <td>GCA</td> <td>GAA</td> <td>стс</td> <td>CTC</td> <td>ССТ</td> <td>aaa</td> <td>CAC</td> <td>כיזיכי</td> <td>አጥሮ</td> <td>990</td>		ТАТ	GAG	GTT	ATG	AAG	מממ	CCA	GCA	GAA	стс	CTC	ССТ	aaa	CAC	כיזיכי	አ ጥሮ	990
344 185 190 195 345 345 346 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG 1038 347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp 200 205 210 348 200 205 210 210 349 200 205 210 210 350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG 1086 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 225 352 215 220 225 353 225 225 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 1134 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 236 230 357 230 235 240 358 CGG ACC CAC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 1182 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 260 360 245 250 361 245 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTC CTC CTC CTC CTC CT			_															330
345 346 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG 347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp 348 350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 352		-1-				_								- 2				
346 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG 1038 347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp 200 Thr Arg Leu Val His His Asn Val Thr Arg Trp 210 349 350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG 1086 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 225 352 215 220 220 353 225 225 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT CAG																		
347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp 348 200 205 210 349 350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG 1086 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 352 215 220 353 225 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 1134 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 1134 356 230 235 240 357 240 358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 1182 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 260 361 245 250 255 260 361 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly		ACA	CGA	CTA	CTG	GAC	ACG	AGA	CTG	GTC	CAC	CAC	AAT	GTG	ACA	CGG	TGG	1038
348 200 205 210 349 350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG 1086 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 225 352 215 220 225 353 225 225 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 1134 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 240 357 230 235 358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 1182 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 250 360 245 250 250 255 255 260 361 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly	347																	
350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG 351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 352 215 220 220 225 225 353 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 356 230 235 235 240 357 358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 360 245	348					~										•	•	
351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys 352 215 220 225 353 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 1134 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 356 230 235 240 357 358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 1182 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 360 245 250 250 255 260 361 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly	349																	
352 215 220 225 353 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 1134 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 356 230 235 240 357 358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 1182 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 360 245 250 255 260 361 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly	350	GAA	ACT	TTT	GAT	GTG	AGC	CCT	GCG	GTC	CTT	CGC	TGG	ACC	CGG	GAG	AAG	1086
353 354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 356 230 235 240 357 358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 360 245 250 250 255 260 361 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly	351	Glu	Thr	Phe	Asp	Val	Ser	Pro	Ala	Val	Leu	Arg	Trp	Thr	Arg	Glu	Lys	
354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT 355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 356 230 235 240 357 358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 360 245 250 250 255 260 361 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly	352			215					220					225	_			
355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr 356	353																	
356	354	CAG	CCA	AAC	TAT	GGG	CTA	GCC	ATT	GAG	GTG	ACT	CAC	CTC	CAT	CAG	ACT	1134
357 358	355	Gln	Pro	Asn	Tyr	Gly	Leu	Ala	Ile	Glu	Val	Thr	His	Leu	His	Gln	Thr	
358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA 359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 360 245 250 255 260 361 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly			230					235					240					
359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln 360 245 250 255 260 361 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly																		
360 245 250 255 260 361 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly																		1182
361 362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly		_	Thr	His	Gln	Gly		His	Val	Arg	Ile		Arg	Ser	Leu	Pro	Gln	
362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC 1230 363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly		245					250					255					260	
363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly																		
																		1230
364 265 270 275		СŢУ	ser	Gly	Asn	_	Ala	Gln	Leu	Arg		Leu	Leu	Val	Thr		Gly	
	304					∠ 05					270					275		

Raw Sequence Listing

04/12/93 13:26:45 S4317.raw

365																	
366	CAT	GAT	GGC	CGG	GGC	CAT	GCC	TTG	ACC	CGA	CGC	CGG	AGG	GCC	AAG	CGT	1278
367				Arg													
368				280					285	3	3	3	3	290	-1-	3	
369																	
370	AGC	CCT	AAG	CAT	CAC	TCA	CAG	CGG	GCC	AGG	AAG	AAG	AAT	AAG	AAC	TGC	1326
371				His													
372			295					300		_	•	•	305	•		•	
373																	
374	CGG	CGC	CAC	TCG	CTC	TAT	GTG	GAC	TTC	AGC	GAT	GTG	GGC	TGG	AAT	GAC	1374
375	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn	Asp	
376	_	310				_	315	_			_	320	_	_		_	
377																	
378	TGG	ATT	GTG	GCC	CCA	CCA	GGC	TAC	CAG	GCC	TTC	TAC	TGC	CAT	GGG	GAC	1422
379	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	Phe	Tyr	Сув	His	Gly	Asp	
380	325					330	_	_			335	_	_		_	340	
381																	
382	TGC	CCC	TTT	CCA	CTG	GCT	GAC	CAC	CTC	AAC	TCA	ACC	AAC	CAT	GCC	ATT	1470
383	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	Ile	
384					345					350					355		
385																	
386	GTG	CAG	ACC	CTG	GTC	AAT	TCT	GTC	AAT	TCC	AGT	ATC	CCC	AAA	GCC	TGT	1518
387	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	Ile	Pro	Lys	Ala	Сув	
388				360					365					370			
389																	
390	TGT	GTG	CCC	ACT	GAA	CTG	AGT	GCC	ATC	TCC	ATG	CTG	TAC	CTG	GAT	GAG	1566
391	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	
392			375					380					385				
393																	
394	TAT	GAT	AAG	GTG	GTA	CTG	AAA	AAT	TAT	CAG	GAG	ATG	GTA	GTA	GAG	GGA	1614
395	Tyr	Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	Val	Val	Glu	Gly	
396		390					395		•			400					
397																	
398				CGC	TGA	SATC	AGG (CAGT	CCTT	GA GO	GATA(GACA(G AT	ATAC	ACAC		1666
399	-	Gly	Сув	Arg													
400	405																
401	a. a.			~- ~~			à.			~~		_~~			~- ~		1506
402	CAC	ACACA	AÇA (CACCA	ACATA	AC A	CAC	ACACA	A CA	JGTT(CCCA	TCC	ACTC	ACC (CACA	CACTAC	1726
403	101	73 CM	aam <i>i</i>	naami	na ma 4	30 M	7030								3 ma		1706
404 405	ACA	SACT	SCT :	rccr.	LATA	SC TO	JGAC".	1.1.1.1.7	A 11.	LAAA	AAAA	AAA	AAAA	AAA A	AATG	AAAAA	1786
406	አ ጥር (י מידיא:	N N C 1	, mma	· COTT	PC: 3/	- - -	, mmm	N TO	· Carrer	רא ממ	TCC	Tr	~~~~ r	ኮጥር እ (CCATAT	1846
407	AIC	CIM	HAC A	AIIC	1CC1.	IG A		41111	A IGA	ACII.	IACG	160	HMM1(311 .	LIGA	CAIAI	1040
408	тсъч	ቦ <i>ር</i> ነው ጥ ፣	י מידמ	իւ ա ւարի	י מיין מב	י מ מ	י מיזי מיז	יאייים	יממיז	ግጥ ልጥኮ	<u> </u>	ממיד	1 2 C 2 2	1	ידיממנ	AAAATG	1906
409	I GA.	- CALI	ain.	(JACH	A A	.nin	LLIM.	. AM	-140	SIMI	IAM	-n-Jru				1300
410	AGT	ידידעי	י ידיים	TTAA	מממ	י ב ב	ממממ	מאמרי	יייט יו	אל אלי.	rcca	CGG	ልልጥጥረ	7			1954
411											- UJA	C G G 2		-			
412																	
413	(2)	INF	ORMA'	rion	FOR	SEO	ID 1	NO:4	:								
414	,																
415			(i) :	SEQUI	ENCE	CHAI	RACTI	ERIS	rics:	:							
416			٠	(A)	LE	NGTH	: 40	am:	ino a	acida	3						

Raw Sequence Listing

04/12/93 13:26:51 S4317.raw

417				(B)	TYI	PE: a	amino	ac:	id							
418				(D)	TO	POTO	3Y: :	linea	ar							
419																
420		(:	ii) 1	MOLE	CULE	TYP	3: p:	rote:	in							
421																
422		(:	ki) S	SEQUI	ENCE	DES	CRIP'	rion:	: SE(QI Ç	NO:	4:				
423																
424	Met	Ile	Pro	Gly	Asn	Arg	Met	Leu	Met	Val	Val	Leu	Leu	Сув	Gln	Val
425	1				5					10					15	
426																
427	Leu	Leu	Gly	Gly	Ala	Ser	His	Ala	Ser	Leu	Ile	Pro	Glu	Thr	Gly	Lys
428				20					25					30		
429																
430	Lys	Lys	Val	Ala	Glu	Ile	Gln	Gly	His	Ala	Gly	Gly	Arg	Arg	Ser	Gly
431			35					40					45			
432																
433	Gln		His	Glu	Leu	Leu	Arg	Asp	Phe	Glu	Ala	Thr	Leu	Leu	Gln	Met
434		50					55					60				
435																
436		Gly	Leu	Arg	Arg	Arg	Pro	Gln	Pro	Ser	_	Ser	Ala	Val	Ile	
437	65					70					75					80
438																
439	Asp	Tyr	Met	Arg	Asp	Leu	Tyr	Arg	Leu		Ser	Gly	Glu	Glu		Glu
440					85					90					95	
441															•	
442	Glu	Gln	Ile		Ser	Thr	Gly	Leu		Tyr	Pro	Glu	Arg		Ala	Ser
443				100					105					110		
444		_														
445	Arg	Ala	Asn	Thr	Val	Arg	Ser		His	His	Glu	Glu		Leu	Glu	Asn
446			115					120					125			
447				_				_	_	_		_				
448	Ile		Gly	Thr	Ser	Glu		Ser	Ala	Phe	Arg		Leu	Phe	Asn	Leu
449		130					135					140				
450	_	_		_		_				_	_			_	_	_
451		Ser	Ile	Pro	GIu		Glu	Val	Ile	Ser		Ala	Glu	Leu	Arg	
452	145					150					155					160
453		_	-1				-1						_			•
454	Pne	Arg	Glu	GIn		Asp	GIN	GIY	Pro	_	Trp	GIu	Arg	GLY		HIS
455					165					170					175	
456	•	-1.	•	-1.	m	~ 3	••- •	**	•				~ 1	•• - 1	••- 3	5
457 458	arg	тте	Asn		ıyr	GIU	val	met	-	Pro	Pro	Ala	GIU		val	LLO
				180					185					190		
459	~ 1	77.5	T	-1 -	m1	3	7	T	3	m1	3	T	17 7	***	77.5	3
460	GTĀ	п18	Leu	тте	inr	Arg	ьeu		ASD	Inr	Arg	ьeu		UIS	nis	ABII
461 462			195					200					205			
462	77~7	ηъ	7		61	πъ	Dh-	7 ~-	17 ~ 7	g	D	21-	17~ T	T	N	Т
464	val		Arg	rrb	GIU	Inr	215	Asp	VAI	ser	PEO		VAI	ьeu	Arg	пр
465		210					413					220				
466	Th∽	A ~~	Glu	Lare	۵1 ت	D~~	A are	Тч	G112	Len	al⇒	TIA	<u>~</u> 1	TeV	Thr	uie
467	225	nr y	GIU	ny s	GIII	230	von	- Y -	GTÄ	Ted	235	TT6	GIU	val	T	240
468	227					250					233					230
700																

Raw Sequence Listing

04/12/93 13:26:52 S4317.raw

469 470 471	Leu	His	Gln	Thr	Arg 245	Thr	His	Gln	Gly	Gln 250	His	Val	Arg	Ile	Ser 255	Arg
472 473 474	Ser	Leu	Pro	Gln 260	Gly	Ser	Gly	Asn	Trp 265	Ala	Gln	Leu	Arg	Pro 270	Leu	Leu
475 476 477	Val	Thr	Phe 275	Gly	His	Asp	Gly	Arg 280	Gly	His	Ala	Leu	Thr 285	Arg	Arg	Arg
478 479 480	Arg	Ala 290	Lys	Arg	Ser	Pro	Lys 295	His	His	Ser	Gln	Arg 300	Ala	Arg	Lys	Lys
481 482 483	Asn 305	Lys	Asn	Сув	Arg	Arg 310	His	Ser	Leu	Tyr	Val 315	Asp	Phe	Ser	Asp	Val 320
484 485 486	Gly	Trp	Asn	Asp	Trp 325	Ile	Val	Ala	Pro	Pro 330	Gly	Tyr	Gln	Ala	Phe 335	Tyr
487 488 489	Сув	His	Gly	Asp 340	Сув	Pro	Phe	Pro	Leu 345	Ala	Asp	His	Leu	Asn 350	Ser	Thr
490 491 492	Asn	His	Ala 355	Ile	Val	Gln	Thr	Leu 360	Val	Asn	Ser	Val	Asn 365	Ser	Ser	Ile
493 494 495	Pro	Lys 370	Ala	Сув	Сув	Val	Pro 375	Thr	Glu	Leu	Ser	Ala 380	Ile	Ser	Met	Leu
496 497 498	Tyr 385	Leu	Asp	Glu	Tyr	Asp 390	Lys	Val	Val	Leu	Lys 395	Asn	Tyr	Gln	Glu	Met 400
499 500 501	Val	Val	Glu	Gly	Сув 405	Gly	Сув	Arg								
502 503 504	(2)	INF(ORMAT			_	ID 1									
505 506 507 508 509		(1,	(1 (1	A) LI 3) TY C) SY	engti YPE : Trani	H: 14 nucl	148 l leic ESS: unki	ase acio doul	pai:	cs						
510 511 512		(ii)	MOI	LECUI	LE T	YPE:	DNA									
513 514 515 516 517		(ix)		A) N2	AME/I		CDS 97.	. 1389	•							
518 519) SE(_					_							
520	GTG	ACCG	AGC (GCG (CGGA	CG G(CCGC	CTGC	CCC	CTCT	GCCA	CCT	3GGG (CGG '	TGCGG	GCCCG

Raw Sequence Listing

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521 522	GAGO	ייררפו	GAG (מפפו	<u>ግር</u> ሞ አ /	3C G	ግር፤ጥ አ	3) CC	- cc	raca	አጥሮ	CAC	CTC	ccc	max.	CTTC	114
523	GAG	CCG	JAG (CCCG	3GIA	3C G(CGIN	JAGC	. GG	JGCG				Arg			114
524											1	1110	Val	Arg	5	пеп	
525											_				-		
526	CGA	GCT	GCG	GCG	CCG	CAC	AGC	TTC	GTG	GCG	CTC	TGG	GCA	CCC	СТС	ттс	162
527			Ala														202
528	5			10					15					20			
529																	
530	CTG	CTG	CGC	TCC	GCC	CTG	GCC	GAC	TTC	AGC	CTG	GAC	AAC	GAG	GTG	CAC	210
531			Arg														
532			25					30					35				
533																	
534	TCG	AGC	TTC	ATC	CAC	CGG	CGC	CTC	CGC	AGC	CAG	GAG	CGG	CGG	GAG	ATG	258
535	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	Gln	Glu	Arg	Arg	Glu	Met	
536		40					45		_			50	_	_			
537																	
538	CAG	CGC	GAG	ATC	CTC	TCC	ATT	TTG	GGC	TTG	CCC	CAC	CGC	CCG	CGC	CCG	306
539	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	Pro	His	Arg	Pro	Arg	Pro	
540	55					60					65					70	
541																	
542			CAG														354
543	His	Leu	Gln	Gly		His	Asn	Ser	Ala		Met	Phe	Met	Leu	Asp	Leu	
544					75					80					85		
545																	
546			GCC														402
547	ıyr	Asn	Ala		АТа	Val	GIU	GIU		GIY	GIY	Pro	GIA		GIn	GIĀ	
548 549				90					95					100			
550	ጥጥር	TCC	TAC	ccc	ጥአ ሮ	አአር	aca	CTC	ጥጥረ	» Ст	N.C.C	CAC	ccc	aaa	CCT	CTC	450
551			Tyr														450
552	2116	Der	105	110	- y -	Lyb	AIG	110	FIIG	Der	1111	GIII	115	FIU	FIU	пеп	
553																	
554	GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC	ATG	GTC	ATG	498
555			Leu														
556		120		_	•		125					130					
557																	
558	AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC	CAC	CCA	CGC	546
559	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	His	Pro	Arg	
560	135					140					145					150	
561																	
562	TAC	CAC	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	CCA	GAA	GGG	594
563	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp		Ser	Lys	Ile	Pro	Glu	Gly	
564					155					160					165		
565													 -				
566			GTC														642
567 568	GIU	Ala	Val		ALA	ALA	GLu	Pue	_	TTE	Tyr	гув	Asp	_	ITE	Arg	
568 560				170					175					180			
569 570	C) N	CGC	TTC	C A C	አአጥ	CA C	A CC	ጥጥ∕ገ	ccc	አጥጣ	N.C.C	Cum	ጥአጥ	CAG	GTP C	CTC	690
570 571			Phe														030
572		3	185	P				190	9		J-3-1		195	U-11			
- · ·																	

Raw Sequence Listing

04/12/93 13:27:12 S4317.raw

573																	
574				TTG													738
575	Gln		His	Leu	Gly	Arg		Ser	Asp	Leu	Phe	Leu	Leu	Asp	Ser	Arg	
576		200					205					210					
577																	
578				GCC													786
579		Leu	Trp	Ala	Ser		Glu	GIA	Trp	Leu		Phe	Asp	Ile	Thr		
580	215					220					225					230	
581				~~~	maa	a ma	ama			~~~			~~~		~~~		224
582				CAC													834
583 584	Thr	ser	ABN	His		val	vaı	ABN	Pro		HIS	ABN	Leu	GIY		GIN	
585					235					240					245		
586	СТС	ሞሮር	CTC	GAG	A C C	СТС	CAT	aaa	CAG	AGC	אידכי	3 3 C	ccc	224	ጥጥ ር	aca	882
587				Glu													862
588	204	501	vul	250		De.	vob	GLY	255	Der	116	ADII	110	260	пец	VIG	
589														200			
590	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	TTC	ATG	GTG	930
591				Gly													200
592	•		265	•	-		•	270			•	_	275	_			
593																	
594	GCT	TTC	TTC	AAG	GCC	ACG	GAG	GTC	CAC	TTC	CGC	AGC	ATC	CGG	TCC	ACG	978
595	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile	Arg	Ser	Thr	
596		280					285					290					
597																	
598	GGG	AGC	AAA	CAG	CGC	AGC	CAG	AAC	CGC	TCC	AAG	ACG	CCC	AAG	AAC	CAG	1026
599	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln	
600	295					300					305					310	
601																	
602				CGG													1074
603				CGG Arg	Met					Glu					Asp		1074
603 604																	1074
603 604 605	Glu	Ala	Leu	Arg	Met 315	Ala	Asn	Val	Ala	Glu 320	Asn	Ser	Ser	Ser	Авр 325	Gln	
603 604 605 606	Glu AGG	Ala	Leu	Arg TGT	Met 315 AAG	Ala AAG	Asn	Val GAG	Ala CTG	Glu 320 TAT	Asn GTC	Ser AGC	Ser TTC	Ser CGA	Asp 325 GAC	Gln CTG	1074 1122
603 604 605 606 607	Glu AGG	Ala	Leu	Arg TGT Cys	Met 315 AAG	Ala AAG	Asn	Val GAG	Ala CTG Leu	Glu 320 TAT	Asn GTC	Ser AGC	Ser TTC	Ser CGA Arg	Asp 325 GAC	Gln CTG	
603 604 605 606 607 608	Glu AGG	Ala	Leu	Arg TGT	Met 315 AAG	Ala AAG	Asn	Val GAG	Ala CTG	Glu 320 TAT	Asn GTC	Ser AGC	Ser TTC	Ser CGA	Asp 325 GAC	Gln CTG	
603 604 605 606 607 608 609	Glu AGG Arg	Ala CAG Gln	Leu GCC Ala	TGT Cys 330	Met 315 AAG Lys	Ala AAG Lys	Asn CAC His	Val GAG Glu	Ala CTG Leu 335	Glu 320 TAT Tyr	Asn GTC Val	Ser AGC Ser	Ser TTC Phe	CGA Arg 340	Asp 325 GAC Asp	Gln CTG Leu	1122
603 604 605 606 607 608 609 610	Glu AGG Arg	Ala CAG Gln TGG	GCC Ala	Arg TGT Cys 330 GAC	Met 315 AAG Lys TGG	Ala AAG Lys ATC	Asn CAC His	Val GAG Glu GCG	Ala CTG Leu 335 CCT	Glu 320 TAT Tyr	Asn GTC Val	Ser AGC Ser	Ser TTC Phe	CGA Arg 340 GCC	Asp 325 GAC Asp	Gln CTG Leu	
603 604 605 606 607 608 609 610	Glu AGG Arg	Ala CAG Gln TGG	GCC Ala CAG Gln	TGT Cys 330	Met 315 AAG Lys TGG	Ala AAG Lys ATC	Asn CAC His	Val GAG Glu GCG Ala	Ala CTG Leu 335 CCT	Glu 320 TAT Tyr	Asn GTC Val	Ser AGC Ser	TTC Phe GCC Ala	CGA Arg 340 GCC	Asp 325 GAC Asp	Gln CTG Leu	1122
603 604 605 606 607 608 609 610 611 612	Glu AGG Arg	Ala CAG Gln TGG	GCC Ala	Arg TGT Cys 330 GAC	Met 315 AAG Lys TGG	Ala AAG Lys ATC	Asn CAC His	Val GAG Glu GCG	Ala CTG Leu 335 CCT	Glu 320 TAT Tyr	Asn GTC Val	Ser AGC Ser	Ser TTC Phe	CGA Arg 340 GCC	Asp 325 GAC Asp	Gln CTG Leu	1122
603 604 605 606 607 608 609 610 611 612 613	Glu AGG Arg GGC Gly	Ala CAG Gln TGG Trp	GCC Ala CAG Gln 345	TGT Cys 330 GAC Asp	Met 315 AAG Lys TGG Trp	AAG Lys ATC Ile	Asn CAC His ATC Ile	GAG Glu GCG Ala 350	Ala CTG Leu 335 CCT Pro	Glu 320 TAT Tyr GAA Glu	Asn GTC Val GGC Gly	AGC Ser TAC	TTC Phe GCC Ala 355	CGA Arg 340 GCC Ala	Asp 325 GAC Asp TAC Tyr	Gln CTG Leu TAC Tyr	1122 1170
603 604 605 606 607 608 609 610 611 612	AGG Arg GGC Gly	Ala CAG Gln TGG Trp	GCC Ala CAG Gln 345	Arg TGT Cys 330 GAC	Met 315 AAG Lys TGG Trp	AAG Lys ATC Ile	CAC His ATC Ile	GAG Glu GCG Ala 350 CCT	Ala CTG Leu 335 CCT Pro	Glu 320 TAT Tyr GAA Glu	Asn GTC Val GGC Gly TCC	AGC Ser TAC Tyr	TTC Phe GCC Ala 355	CGA Arg 340 GCC Ala	Asp 325 GAC Asp TAC Tyr	Gln CTG Leu TAC Tyr	1122
603 604 605 606 607 608 609 610 611 612 613 614	AGG Arg GGC Gly	Ala CAG Gln TGG Trp	GCC Ala CAG Gln 345	TGT Cys 330 GAC Asp	Met 315 AAG Lys TGG Trp	AAG Lys ATC Ile	CAC His ATC Ile	GAG Glu GCG Ala 350 CCT	Ala CTG Leu 335 CCT Pro	Glu 320 TAT Tyr GAA Glu	Asn GTC Val GGC Gly TCC	AGC Ser TAC Tyr	TTC Phe GCC Ala 355	CGA Arg 340 GCC Ala	Asp 325 GAC Asp TAC Tyr	Gln CTG Leu TAC Tyr	1122 1170
603 604 605 606 607 608 609 610 611 612 613 614 615	AGG Arg GGC Gly	Ala CAG Gln TGG Trp GAG Glu	GCC Ala CAG Gln 345	TGT Cys 330 GAC Asp	Met 315 AAG Lys TGG Trp	AAG Lys ATC Ile	CAC His ATC Ile	GAG Glu GCG Ala 350 CCT	Ala CTG Leu 335 CCT Pro	Glu 320 TAT Tyr GAA Glu	Asn GTC Val GGC Gly TCC	AGC Ser TAC Tyr	TTC Phe GCC Ala 355	CGA Arg 340 GCC Ala	Asp 325 GAC Asp TAC Tyr	Gln CTG Leu TAC Tyr	1122 1170
603 604 605 606 607 608 609 610 611 612 613 614 615 616	Glu AGG Arg GGC Gly TGT Cys	CAG Gln TGG Trp GAG Glu 360	GCC Ala CAG Gln 345 GGG Gly	TGT Cys 330 GAC Asp	Met 315 AAG Lys TGG Trp TGT Cys	Ala AAG Lys ATC Ile GCC Ala	CAC His ATC Ile TTC Phe 365	GAG Glu GCG Ala 350 CCT Pro	Ala CTG Leu 335 CCT Pro	Glu 320 TAT Tyr GAA Glu AAC Asn	Asn GTC Val GGC Gly TCC Ser	AGC Ser TAC Tyr TAC Tyr 370	TTC Phe GCC Ala 355 ATG Met	CGA Arg 340 GCC Ala AAC	Asp 325 GAC Asp TAC Tyr GCC Ala	CTG Leu TAC Tyr	1122 1170
603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619	Glu AGG Arg GGC Gly TGT Cys AAC Asn	CAG Gln TGG Trp GAG Glu 360 CAC	GCC Ala CAG Gln 345 GGG Gly	TGT Cys 330 GAC Asp GAG Glu	Met 315 AAG Lys TGG Trp TGT Cys	Ala AAG Lys ATC Ile GCC Ala CAG	Asn CAC His ATC Ile TTC Phe 365	GAG Glu GCG Ala 350 CCT Pro	Ala CTG Leu 335 CCT Pro CTG Leu GTC	Glu 320 TAT Tyr GAA Glu AAC Asn	Asn GTC Val GGC Gly TCC Ser	AGC Ser TAC Tyr TAC Tyr 370	TTC Phe GCC Ala 355 ATG Met	CGA Arg 340 GCC Ala AAC Asn	Asp 325 GAC Asp TAC Tyr GCC Ala	CTG Leu TAC Tyr ACC Thr	1122 1170 1218
603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620	Glu AGG Arg GGC Gly TGT Cys	CAG Gln TGG Trp GAG Glu 360 CAC	GCC Ala CAG Gln 345 GGG Gly	TGT Cys 330 GAC Asp GAG Glu	Met 315 AAG Lys TGG Trp TGT Cys	Ala AAG Lys ATC Ile GCC Ala CAG	Asn CAC His ATC Ile TTC Phe 365 ACG	GAG Glu GCG Ala 350 CCT Pro	Ala CTG Leu 335 CCT Pro CTG Leu GTC	Glu 320 TAT Tyr GAA Glu AAC Asn	Asn GTC Val GGC Gly TCC Ser	AGC Ser TAC Tyr TAC Tyr 370	TTC Phe GCC Ala 355 ATG Met	CGA Arg 340 GCC Ala AAC Asn	Asp 325 GAC Asp TAC Tyr GCC Ala	CTG Leu TAC Tyr ACC Thr	1122 1170 1218
603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621	Glu AGG Arg GGC Gly TGT Cys AAC Asn 375	CAG Gln TGG Trp GAG Glu 360 CAC	GCC Ala CAG Gln 345 GGG Gly GCC Ala	TGT Cys 330 GAC Asp GAG Glu	Met 315 AAG Lys TGG Trp TGT Cys	Ala AAG Lys ATC Ile GCC Ala CAG Gln 380	CAC His ATC Ile TTC Phe 365 ACG Thr	GAG Glu GCG Ala 350 CCT Pro	Ala CTG Leu 335 CCT Pro CTG Leu GTC Val	Glu 320 TAT Tyr GAA Glu AAC ABN	Asn GTC Val GGC Gly TCC Ser TTC Phe 385	AGC Ser TAC Tyr TAC Tyr 370 ATC	TTC Phe GCC Ala 355 ATG Met	CGA Arg 340 GCC Ala AAC ASN	Asp 325 GAC Asp TAC Tyr GCC Ala GAA Glu	CTG Leu TAC Tyr ACC Thr ACG Thr 390	1122 1170 1218 1266
603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 620 621 622	Glu AGG Arg GGC Gly TGT Cys AAC Asn 375 GTG	CAG Gln TGG Trp GAG Glu 360 CAC His	GCC Ala CAG Gln 345 GGG Gly GCC Ala	TGT Cys 330 GAC Asp GAG Glu ATC Ile	Met 315 AAG Lys TGG Trp TGT Cys GTG Val	Ala AAG Lys ATC Ile GCC Ala CAG GIn 380 TGT	Asn CAC His ATC Ile TTC Phe 365 ACG Thr	GAG Glu GCG Ala 350 CCT Pro CTG Leu CCC	Ala CTG Leu 335 CCT Pro CTG Leu GTC Val	Glu 320 TAT Tyr GAA Glu AAC ABN CAC His	Asn GTC Val GGC Gly TCC Ser TTC Phe 385 CTC	AGC Ser TAC Tyr 370 ATC Ile	TTC Phe GCC Ala 355 ATG Met AAC Asn	CGA Arg 340 GCC Ala AAC ABN CCG Pro	Asp 325 GAC Asp TAC Tyr GCC Ala GAA Glu	CTG Leu TAC Tyr ACC Thr ACG Thr 390	1122 1170 1218
603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621	Glu AGG Arg GGC Gly TGT Cys AAC Asn 375 GTG	CAG Gln TGG Trp GAG Glu 360 CAC His	GCC Ala CAG Gln 345 GGG Gly GCC Ala	TGT Cys 330 GAC Asp GAG Glu	Met 315 AAG Lys TGG Trp TGT Cys GTG Val	Ala AAG Lys ATC Ile GCC Ala CAG GIn 380 TGT	Asn CAC His ATC Ile TTC Phe 365 ACG Thr	GAG Glu GCG Ala 350 CCT Pro CTG Leu CCC	Ala CTG Leu 335 CCT Pro CTG Leu GTC Val	Glu 320 TAT Tyr GAA Glu AAC ABN CAC His	Asn GTC Val GGC Gly TCC Ser TTC Phe 385 CTC	AGC Ser TAC Tyr 370 ATC Ile	TTC Phe GCC Ala 355 ATG Met AAC Asn	CGA Arg 340 GCC Ala AAC ABN CCG Pro	Asp 325 GAC Asp TAC Tyr GCC Ala GAA Glu	CTG Leu TAC Tyr ACC Thr ACG Thr 390	1122 1170 1218 1266

Raw Sequence Listing

04/12/93 13:27:18 S4317.raw

625																	
626	CTC	TAC	TTC	GAT	GAC	AGC	TCC	AAC	GTC	ATC	CTG	AAG	AAA	TAC	AGA	AAC	1362
627	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	
628				410					415					420			
629																	
630				CGG						TAG	CTCC'	ICC (GAGA	ATTC	AG		1409
631	Met	Val	Val	Arg	Ala	Сув	Gly	Сув	His								
632			425					430									
633																	
634	ACC	CTTT	GGG	GCCA	AGTT'	TT T	CTGG	ATCC:	r cc	ATTG	CTC						1448
635																	
636																	
637	(2)	INF	ORMA	TION	FOR	SEQ	ID 1	NO: 6	:								
638																	
639			(i)	SEQU	ENCE	CHA	RACT	ERIS:	rics	:							
640				(A)) LE	NGTH	: 43	l am:	ino a	acid	8						
641				(B)	TY:	PE: a	amino	ac:	id								
642				(D	TO	POTO	GY: :	linea	ar								
643																	
644		(:	ii)	MOLE	CULE	TYP	E: p	rote:	in								
645																	
646		(:	xi)	SEQU	ence	DES	CRIP:	CION	: SE	Q ID	NO:	6:					
647																	
648	Met	His	Val	Arg	Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala	
649	1				5					10					15		
650																	
651	Leu	Trp	Ala	Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser	
652				20					25					30			
653																	
654	Leu	Asp	Asn	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	
655			35					40					45				
656																	
657	Gln	Glu	Arg	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	
658		50					55					60					
659																	
660	Pro	His	Arg	Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	
661	65					70					75					80	
662																	
663	Met	Phe	Met	Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	
664					85					90					95		
665																	
666	Gly	Pro	Gly	Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	
667				100					105					110			
668																	
669	Thr	Gln	_	Pro	Pro	Leu	Ala		Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	
670			115					120					125				
671																	
672	Asp		Asp	Met	Val	Met		Phe	Val	Asn	Leu		Glu	His	Asp	Lys	
673		130					135					140					
674					_												
675		Phe	Phe	His	Pro	_	Tyr	His	His	Arg		Phe	Arg	Phe	Asp		
676	145					150					155					160	

Raw Sequence Listing

04/12/93 13:27:25 S4317.raw

688																
677 678	a	T	71.	D	~1	~1	~1		77-7	m1	.1.		~1	51		
678	ser	гля	Ile	PTO		GIY	GIU	Ala	vai		ALA	Ата	GIU	Pne	_	ITe
679					165					170					175	
680	_	_	_	_		_		_		_						_
681	Tyr	Lys	Asp		Ile	Arg	Glu	Arg		Asp	Asn	Glu	Thr		Arg	Ile
682				180					185					190		
683																
684	Ser	Val	Tyr	Gln	Val	Leu	Gln		His	Leu	Gly	Arg	Glu	Ser	Asp	Leu
685			195					200					205			
686																
687	Phe		Leu	Asp	Ser	Arg		Leu	\mathtt{Trp}	Ala	Ser	Glu	Glu	Gly	\mathtt{Trp}	Leu
688		210					215					220				
689																
690	Val	Phe	Asp	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg
691	225					230					235					240
692																
693	His	Asn	Leu	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser
694					245					250					255	
695																
696	Ile	Asn	Pro	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn
697				260					265	_	_		_	270		
698																
699	Lys	Gln	Pro	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe
700	_		275					280		•			285			
701																
702	Arg	Ser	Ile	Arq	Ser	Thr	Gly	Ser	Lys	Gln	Arq	Ser	Gln	Asn	Arq	Ser
703		290					295		•			300				
704																
705	Lys	Thr	Pro	Lys	Asn	Gln	Glu	Ala	Leu	Arq	Met	Ala	Asn	Val	Ala	Glu
706	305			•		310				-	315					320
707																
708	Asn	Ser	Ser	Ser	asp	Gln	Ara	Gln	Ala	Cvs	Lvs	Lvs	His	Glu	Leu	Tvr
709					325					330					335	-1-
710																
711	Val	Ser	Phe	Ara	Asp	Leu	Glv	Trp	Gln	asp	Trp	Ile	Ile	Ala	Pro	Glu
712				340			1		345	E				350		
713																
714	Glv	Tvr	Ala	λla	Tvr	Tvr	Cvs	Glu	Glv	Glu	Cvs	Ala	Phe	Pro	Leu	Aan
715	1	-1-	355		-1-	-1-	-7-	360	4-1		- 7.5		365			
716			-					500					J 0 J			
717	Ser	Тугт	Met	λen	Δla	Thr	λen	Wie	ב [ג	Tla	17 a 1	Gln	Thr	T.011	V=3	Wie
718	561	370	Mec	ADII	nia		375		AIG	116	Val	380	1111	пец	Val	1110
719		3,0					3,3					300				
720	Pho	T3.0	Asn	D~~	G1.,	The	77 o T	Dro	Tara	Dro	Cara	Crea	7 T n	Dro	Th-	C1 n
721	385		VOII	-10	GIU	390	AGT	-10	מעת	-10	395	CYB	ATA	FIO	TILL	400
721	303					J 9 U					333					-100
723	Lou	λ c ~	7 J ~	T1 ^	G^~	17 n 1	Low	т	Dha	λ c=	λ c=	e~~	g.~	λ	17-7	т1 -
724	neu	ASII	Ala	тта	405	AGT	пеп	TÄL	rne	_	wsb	ser.	ser	ABII	415	тте
725					#UD					410					4 T D	
725 726	T	T	Lys	т	7 ∽ ~	7	Wa-	1707	37~7	λ	37 -	~·-	61	~	u: -	
725 727	теп	пЛв	тЛв	_	Arg	ABN	met	val		Arg	WTG	CAR	GTÅ	-	п18	
				420					425					430		
728																

Raw Sequence Listing

04/12/93 13:27:32 S4317.raw

149	(Z) INFO	RMAIION FOR SEQ ID NO:/:
730		
731	(1)	SEQUENCE CHARACTERISTICS:
732		(A) LENGTH: 2923 base pairs
733		(B) TYPE: nucleic acid
734		(C) STRANDEDNESS: double
735		(D) TOPOLOGY: circular
736		
737	(ii)	MOLECULE TYPE: cDNA to mRNA
738		
739	(iii)	HYPOTHETICAL: NO
740		
741	(vi)	ORIGINAL SOURCE:
742		(A) ORGANISM: Homo sapiens
743		(F) TISSUE TYPE: Human placenta
744		
745	(vii)	IMMEDIATE SOURCE:
746		(A) LIBRARY: Stratagene catalog #936203 Human placenta
747		cDNA library
748		(B) CLONE: BMP6C35
749		
750	(viii)	POSITION IN GENOME:
751		(C) UNITS: bp
752		
753	(ix)	FEATURE:
754		(A) NAME/KEY: CDS
755		(B) LOCATION: 1601701
756		
757	(ix)	FEATURE:
758		(A) NAME/KEY: mat_peptide
759		(B) LOCATION: 12821698
760		
761	(1x)	FEATURE:
762		(A) NAME/KEY: mRNA
763		(B) LOCATION: 12923
764		
765	(GROWENGE REGERENCE GEO. TR. VO. F.
766 767	(X1)	SEQUENCE DESCRIPTION: SEQ ID NO:7:
768	GG3 GG3 MG	
	CGACCATG	AG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCC GAGAGGTGGC 60
769	accar and	TM 020002200 000202000 000000000 00000000
770 771	GGGGACTG	CT CACGCCAAGG GCCACAGCGG CCGCGCTCCG GCCTCGCTCC GCCGCTCCAC 120
772	CCCTCCCC	TO ATTOCOMORGO COACOMORGO COCOMORGO ATTO COM COM CTO COM
773	GCCTCGCG	GG ATCCGCGGGG GCAGCCCGGC CGGGCGGGG ATG CCG GGG CTG GGG 174 Met Pro Gly Leu Gly
774		-374 -370
775		-3/4 -3/0
776	CCC NCC	GCG CAG TGG CTG TGC TGG TGG TGG GGG CTG CTG TGC AGC TGC 222
777		
778	Ary Ary	Ala Gln Trp Leu Cys Trp Trp Gly Leu Leu Cys Ser Cys -365 -360 -355
779		-300 -303
780	דפר פפפ י	CCC CCG CCG CTG CGG CCC TTG CCC GCT GCC GCG GCC GCC
, 50	19C 999 (270

Raw Sequence Listing

04/12/93 13:27:39 S4317.raw

781	Cys	Gly	Pro	Pro		Leu	Arg	Pro			Pro	Ala	Ala			Ala	
782				-350)				-34	5				-340)		
783																	
784				GGG													318
785	Ala	АТА	_	Gly	GIn	Leu	Leu	_	_	GТĀ	GIY	Ser			Arg	Thr	
786			-33	>				-33(כ				-32	•			
787																	
788				CCG													366
789	Glu			Pro	Pro	Ser			Ser	Ser	Ser	_		Leu	Tyr	Arg	
790		-320)				-31	5				-31)				
791																	
792				ACG													414
793	_		Lys	Thr	Gln		_	Arg	Glu	Met		_	Glu	Ile	Leu		
794	-30!	5				-300	כ				-29!	5				-290	
795																	
796				CTC													462
797	Val	Leu	Gly	Leu			Arg	Pro	Arg			His	Gly	Leu			
798					-28	5				-280)				-275	5	
799																	
800				CCG													510
801	Pro	Gln	Pro	Pro		Leu	Arg	Gln			Glu	Gln	Gln			Gln	
802				-270	ס				-26	5				-260)		
803																	
804				CGC													558
805	Gln	Leu		Arg	Gly	Glu	Pro			Gly	Arg	Leu	_		Ala	Pro	
806			-25	5				-250)				-245	5			
807																	
808				CTG													606
809	Leu			Leu	Asp	Leu	-		Ala	Leu	Ser		-	Asn	Asp	Glu	
810		-240)				-235	5				-23)				
811																	
812				TCG													654
813	_	_	Ala	Ser	Glu	_		Arg	Gln	Gln		_	Pro	His	Glu		
814	-22!	5				-220	ט				-21!	5				-210	
815																	
816				TCC													702
817	Ala	Ser	Ser	Ser		_	Arg	GIn	Pro			GIA	Ala	Ala			
818					-20	•				-200	,				-195	•	
819	ama		~~~			amm	ama		~~~	aa .		~~~			~~~	999	750
820				AAG													750
821	Leu	Asn	Arg	Lys		Leu	Leu	Ala		_	ser	GIĀ	ser		_	Ala	
822				-190	J				-18	•				-180	,		
823	maa	003	ama.	3.00	3.00	~~~	a. a	a. a	300	000	mma	ama	330	a. a	000	ara.	700
824				ACC													798
825	ser	PTO		Thr	ser	ATG	GIN	ASP -17(ATS	rne	neu		_	ATS	vab	
826			-17!	,				-1/(J				-16	,			
827	3 mc	ama.	7 m/	300	mmm	ama	224	CITIC	ama	C2 C	መልጣ	CNC	224	C A C	mm/	TCC	846
828 829				AGC													010
	met			Ser	rne	val	-155		AST	GIU	тÀĽ	-15	_	GIU	rne	Ser	
830 831		-160	,				-TD:	,				-13	,				
832	CCT	CGT	CAC	CGA	C2 C	מאמ	2 2 2	GN C	ጥጥረ	<u>አ</u> አሮ	ար	אאמ	מ יחידו	TCC	CAG	ልጥጥ	894
034	CCI	CGI	CAG	CGA	CAC	-AC	nnn	UAU	110	DAG	110	AAC	TIM	100	CAG	ni.	037

Raw Sequence Listing

04/12/93 13:27:45 S4317.raw

833 834 835	Pro -14	Arg 5	Gln	Arg	His	His -14	-	Glu	Phe	Lys	Phe -13!		Leu	Ser	Gln	Ile -130	
836	CCT	GAG	GGT	GAG	GTG	GTG	ACG	GCT	GCA	GAA	TTC	CGC	ATC	TAC	AAG	GAC	942
837	Pro	Glu	Gly	Glu			Thr	Ala	Ala			Arg	Ile	Tyr	Lys	Asp	
838					-12!	5				-120	כ				-11!	5	
839				~~~													
840		GTT															990
841 842	Сув	Val	Met	-11		Pne	гĀ8	ABN	-10!		Pne	Leu	TTE			ıyr	
843				-11(,				-10:	•				-100	J		
844	CAA	GTC	тта	CAG	GAG	САТ	CAG	CAC	AGA	GAC	тст	GAC	СТС	ጥጥጥ	ጥጥር	ጥጥር	1038
845		Val															1030
846			-95					-90	3				-85				
847																	
848	GAC	ACC	CGT	GTA	GTA	TGG	GCC	TCA	GAA	GAA	GGC	TGG	CTG	GAA	TTT	GAC	1086
849	Asp	Thr	Arg	Val	Val	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Glu	Phe	Asp	
850		-80					-75					-70					
851																	
852		ACG															1134
853		Thr	Ala	Thr	Ser		Leu	Trp	Val	Val		Pro	Gln	His	Asn		
854 855	-65					-60					-55					-50	
856	GGG	CTT	CAG	CTC	» CC	GTG.	CTC	A C A	NGG	CAT	CCA	GTC	CAC	CTC	CAC	ccc	1182
857		Leu															1102
858	,				-45				5	-40	U-7				-35		
859																	
860	CGA	GCC	GCA	GGC	CTG	GTG	GGC	AGA	GAC	GGC	CCT	TAC	GAT	AAG	CAG	CCC	1230
861	Arg	Ala	Ala	Gly	Leu	Val	Gly	Arg	Asp	Gly	Pro	Tyr	Asp	Lys	Gln	Pro	
862				-30					-25					-20			
863																	
864		ATG															1278
865	Phe	Met		Ala	Phe	Phe	Lys		Ser	Glu	Val	His	_	Arg	Thr	Thr	
866			-15					-10					-5				
867 868	» GG	TCA	GCC	TCC	NGC	ccc	ccc	CCA	CAA	CNG	አርጥ	ССТ	አአጥ	cac	ጥረጥ	N.C.C	1326
869		Ser															1320
870	9	1		50-		5	9	9			10	9		9		15	
871																	
872	CAG	TCC	CAG	GAC	GTG	GCG	CGG	GTC	TCC	AGT	GCT	TCA	GAT	TAC	AAC	AGC	1374
873	Gln	Ser	Gln	Asp	Val	Ala	Arg	Val	Ser	Ser	Ala	Ser	Asp	Tyr	Asn	Ser	
874					20					25					30		
875																	
876		GAA															1422
877	Ser	Glu	Leu	_	Thr	Ala	Cys	Arg	_	His	Glu	Leu	Tyr		ser	Phe	
878 879				35					40					45			
879 880	CAA	GAC	CTC	GG3	тсс	CAG	CAC	тес	አ ጥሮ	אַריי	GC »	רככ	AAG	מפר	тат	ርር ጥ	1470
881		Asp															14,0
882			50	1			E	55					60	3	-1-		
883																	
884	GCC	AAT	TAC	TGT	GAT	GGA	GAA	TGC	TCC	TTC	CCA	CTC	AAC	GCA	CAC	ATG	1518

Raw Sequence Listing

04/12/93 13:27:52 S4317.raw

885 886 887	Ala	Asn 65	Tyr	Сув	Asp	Gly	Glu 70	Сув	Ser	Phe	Pro	Leu 75	Asn	Ala	His	Met	
888	AAT	GCA	ACC	AAC	CAC	GCG	ATT	GTG	CAG	ACC	TTG	GTT	CAC	CTT	ATG	AAC	1566
889	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Asn	
890	80					85					90					95	
891																	
892	CCC	GAG	TAT	GTC	CCC	AAA	CCG	TGC	TGT	GCG	CCA	ACT	AAG	CTA	AAT	GCC	1614
893	Pro	Glu	Tyr	Val	Pro	Lys	Pro	Cys	Сув	Ala	Pro	Thr	Lys	Leu	Asn	Ala	
894					100					105					110		
895																	
896	ATC	TCG	GTT	CTT	TAC	TTT	GAT	GAC	AAC	TCC	AAT	GTC	ATT	CTG	AAA	AAA	1662
897	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Asn	Ser	Asn	Val	Ile	Leu	Lys	Lys	
898				115					120					125			
899																	
900	TAC	AGG	AAT	ATG	GTT	GTA	AGA	GCT	TGT	GGA	TGC	CAC	TAAC	CTCG	AAA		1708
901	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala	Сув	Gly	Сув	His					
902			130					135					140				
903																	
904	CCA	ATG	CTG	GGGA	CACA	CA T	CTG	CTTC	GA'	rtcc:	raga	TTAC	CATC	rgc	CTTAI	AAAAA	A 1768
905																	
906	CAC	GAA(SCA	CAGT	rgga(G T	EGGA (CGAT	AG2	ACTT!	rgaa	ACT	ATCT	CAT	GCCA	GTGCC:	r 1828
907																	
908	TAT	CACC	CAG	GAAG	ATTT:	CA A	AGGA	CTC	A TT	AATA	ATTT	GCT	CACT	rgg	TAAA'	rgacg:	r 1888
909																	
910	GAG	'AGT'	rgt	TGGT	CTGT	AG C	AAGC	rgag'i	TTC	GAT(STCT	GTA	SCAT	AAG	GTCT	GTAA (1948
911																	
912	TGC	\GAA	AÇA	TAAC	CGTG	AA G	CTCT	CCT	CCC	CTCC	rccc	CCA	AAAA(CCC	ACCA	AAATT	A 2008
913																	
914	GTTT	TAG	CTG	TAGA	rcaa(C T	ATTTC	:GGG'	r GT	rtgt:	ragt	AAA'	ragg	3AA	AATA	ATCTC	A 2068
915	3300	13 Am		3 mam:	mmor	nm (1	70M3.7			. aama		~ ~ ~	n 2 cm/	3ma	m. ma		. 0100
916 917	AAG	AGT.	ľAA	ATGT	ATTC:	L'I' G(3CTA	iagg/	i TC	AGCT	3GTT	CAG.	racte	FIC	TATC	AAAGG:	r 2128
918	አሮአባ	rmmm 7		CACA			פר כי	77777	T TO CO	7000	7777	acar	namar	nma	a comme	CATTC	2188
919	AGA.		CA	GAGAZ	ACAGI	M A.	CGGC	JAAC	3 IG() 	SAAC	GCC.	LCIG.	iic	AGII	LATIC	2100
920	CAGI	አ ረታጥ (ירא	CNGG	A CCC	\C \ \(\)	בכככז	cece	י ארי	, מממז	A CCC	CTC/	יז ממי	200	cece	CTTGT	2248
921	CAG	WG1(-CA	CAGG	10002	ic a	30002	1996	. AC	1000	1000	CIC	JAC G	366	CGCC	CIIGI	2270
922	ጥር እ ር	ימיחיב	רידיכו	כיויכיויי	ימייטיו	רכו ידי	ייינייי	ברדננ	י אכי	րդորդու	<u> </u>	CTC	ו מ מים	ላ አጥ	אראכי	TATT:	г 2308
923	1040	J. C.	. 1 3	CIGI.	IGIA.		CGIC	CIGO	, AG.		3110	GIG.	CAL		ACAC.	LIALL.	2500
924	CAGO	CAAZ	AAC	ATAC	ייייע	רכי די	ACACO	тсал	ТСС	יייי ביייי	ላ ጥጥጥ	GCTC	מיים בייני	rcm	ттсс	ragta(2368
925	01101											UU21					
926	CAAZ	AGT	AGA	CTGAT	TAC!	AC TO	GAGG	rgago	CT	ACAAC	GGG	TGT	GTAA(CCG	TGTA	ACACG:	r 2428
927																	
928	GAAG	GCA	FTG	CTCA	CCTC	CT C	CTTAC	CAG	AC	GTT	CTTT	GAC	CAGC	ACA	TTAA	CTTCT	3 2488
929																	
930	GACT	rgcc	GC.	TCTAC	GTAC	T T	TCAC	TAA	A GT	GTT	CTCT	GCC.	TTTT:	TAC	TATA	CAGCA:	r 2548
931																	
932	ACC	ACGC	CAC	AGGG	TAG!	AA C	CAAC	SAAG	AA	ATAAI	AATG	AGG	GTGC	CCA	GCTT	ATAAG	A 2608
933																	
934	ATG	TGT	ľAG	GGGGZ	ATGA	C A	rgcto	TTT	A TG	AACG	AAAE	TCA:	rgat:	ГТС	CCTG:	FAGAA	A 2668
935																	
936	GTG	AGGC1	CA	GATT	TAAA	CT T	AGAA!	TTTAT	TC	'AAA'	rgtc	TTT:	TTCA	CAA	TCAT	GTGAC:	r 2728

Raw Sequence Listing

04/12/93 13:27:53 S4317.raw

937		
938 939	GGGAAGGCAA TTTCATACTA AACTGATTAA ATAATACATT TATAATCTAC AACTGTTTGC	2788
940	2 CTT2 C2 CCT TTTTTTTTTTT 2 2 T 2 T 2 T	0040
941	ACTTACAGCT TTTTTTGTAA ATATAAACTA TAATTTATTG TCTATTTTAT ATCTGTTTTG	2848
941	CDCDCCCCDD CCCCCCCCCCCCCCDDDDD CCCCCCCC	
943	CTGTGGCGTT GGGGGGGGG CCGGGCTTTT GGGGGGGG	2908
943		
945	GGTGTGGGCG GGCGG	2923
946		
947	(2) THEODWANTON HOD GEO TO NO. 0.	
948	(2) INFORMATION FOR SEQ ID NO:8:	
949	(1) GEOVERNOE OVER OMERICANICA	
950	(i) SEQUENCE CHARACTERISTICS:	
950 951	(A) LENGTH: 513 amino acids	
951 952	(B) TYPE: amino acid (D) TOPOLOGY: linear	
952 953	(D) TOPOLOGI: Tinear	
953 954	(ii) MOI EGII E MUDE, probain	
955	(ii) MOLECULE TYPE: protein	
956	(1) GEOMENGE DEGGDIDMION, GEO. ID NO. 0.	
950 957	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
95 <i>1</i> 958	Wet Dee Clarter Clarter and also Clarter Terr Con Many Many Many Clar	
959	Met Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys Trp Trp Gly -374 -370 -365 -360	
960	-374 -370 -365 -360	
961	Tou Tou Gra Con Chia Chia Clir Dro Dro Dro Lou Ana Dro Dro Tou Dro	
962	Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro -355 -350 -345	
963	-335 -350 -345	
964	Ala Ala Ala Ala Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly	
965	-340 -335 -330	
966	-340 -335 -330	
967	Ser Pro Gly Arg Thr Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser	
968	-325 -320 -315	
969	-323 -320 -313	
970	Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln	
971	-310 -305 -300 -295	
972	-303 -300 -255	
973	Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu	
974	-290 -285 -280	
975	200	
	His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu	
977	-275 -270 -265	
978	-/·	
979	Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg	
980	-260 -255 -250	
981		
982	Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser	
983	-245 -240 -235	
984		
985	Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser	
986	-230 -225 -220 -215	
987		
988	Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro	

Raw Sequence Listing

04/12/93 13:28:06 S4317.raw

989					-21	0				-20	05				- 2	200
990																
991	Gly	Ala	Ala	His	Pro	Leu	Asn	Arg	Lys	Ser	Leu	Leu	Ala	Pro	Gly	Ser
992				-19	5				-19	90				-:	185	
993																
994	Gly	Ser	Gly	Gly	Ala	Ser	Pro	Leu	Thr	Ser	Ala	Gln	Asp	Ser	Ala	Phe
995			-180	0				-17	75				-:	170		
996																
997	Leu	Asn	Asp	Ala	Asp	Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	Tvr
998		-169			•		-10						L55			
999												-				
1000	asa	Lvs	Glu	Phe	Ser	Pro	Ara	Gln	Ara	His	His	Lvs	Glu	Phe	Lys	Phe
1001	-15					-14	_		5			L40			-10	-135
1002						•	• •				•					- 133
1003	Agn	T.011	Cor	Gln.	Tla	Pro	G 111	Glar	G1.,	Wa 1	77-1	Th.	21-	212	Glu	Dho
1003	ADII	пеп	Ser	GIII	-130		GIU	GIY	GIU	-12		1111	ATG	ALG		L20
1005					-13	,				-14	23					120
1005	3	71 0	TT	T	3 am	~	171	Wa.	a 1	a	Dh.	T	3	a 1	m1	nh -
	Arg	TTG	IAL	-11!		САВ	vaı	mec	_		Pne	гЛя	ABN		Thr	Pne
1007				-11:	•				-11	LU					105	
1008		-1-	~	-1.		~ 1	7		41	~ 3	•		•	_	_	_
1009	ren	TTE			ıyr	GIN	vaı			GIU	HIS	Gin		_	Asp	Ser
1010			-100	J				- 9!	5				-90)		
1011	_	_		_	_	_		_			_		_			
1012	Asp		Phe	Leu	Leu	Asp		Arg	Val	Val	\mathtt{Trp}		Ser	Glu	Glu	Gly
1013		-85					-80					-75				
1014																
1015	_	Leu	Glu	Phe	Asp		Thr	Ala	Thr	Ser		Leu	Trp	Val	Val	
1016	-70					-65					-60					-55
1017																
1018	Pro	Gln	His	Asn	Met	Gly	Leu	Gln	Leu	Ser	Val	Val	Thr	Arg	Asp	Gly
1019					-50					-45					-40	
1020																
1021	Val	His	Val	His	Pro	Arg	Ala	Ala	Gly	Leu	Val	Gly	Arg	Asp	Gly	Pro
1022				-35					-30					-25		
1023																
1024	Tyr	Asp	Lys	Gln	Pro	Phe	Met	Val	Ala	Phe	Phe	Lys	Val	Ser	Glu	Val
1025			-20					-15					-10			
1026																
1027	His	Val	Arg	Thr	Thr	Arg	Ser	Ala	Ser	Ser	Arg	Arg	Arg	Gln	Gln	Ser
1028		-5	_			_	1				5	_	_			10
1029																
1030	Arg	Asn	Arg	Ser	Thr	Gln	Ser	Gln	Asp	Val	Ala	Arg	Val	Ser	Ser	Ala
1031	_		_		15				-	20		_			25	
1032					,											
1033	Ser	Asp	Tvr	Asn	Ser	Ser	Glu	Leu	Lvs	Thr	Ala	Cvs	Ara	Lvs	His	Glu
1034		- 45-		30					35			- 2 -		40		
1035																
1036	Lev	Tvr	Va l	Ser	Phe	Gln	Agn	Len	G] v	Tro	Gln	Agn	Trn	Πle	Ile	Ala
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1039	Pro	Lve	Glv	Tvr	Δ 1 =	Al a	Δgn	ጥረታ	Cva	Δρη	ദ്രാഹ	GI 11	Care	Ser	Phe	Pro
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Raw Sequence Listing

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1042	1041												
1043 75 80 85 90 1044 1045 Val His Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro 1046 95 100 105 1047 1048 Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn 1049 110 115 120 1050 1051 Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys 1052 125 130 135 1054 His 1055 1056 1057 (2) INFORMATION FOR SEQ ID NO:9: 1059 (3) SEQUENCE CHARACTERISTICS: 1061 (A) LENGTH: 2153 base pairs (B) TypE: nucleic acid (C) STRANDENDENSS: double (D) TOPOLOGY: linear (A) Cys TypE (A) Cys 1066 1066 (iii) HYPOTHETICAL: NO 1067 (Vi) ORIGINAL SOURCE: 1069 (A) ORGANISM: Homo sapiens (H) CELL LINE: U2-OS osteosarcoma (DNA library 1074 (B) CLONE: U2-16 1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library (B) CLONE: U2-16 1076 (Viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 (ix) FEATURE: 1084 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1086 (ix) FEATURE: 1086 (ix) FEATURE: 1087 (A) NAME/KEY: mat_peptide 1088 (ix) FEATURE: 1089 (B) LOCATION: 16472060		I.eu Agn	Ala Hig Mot	Agn Ala	Thr 2	Aan E	ui a	λl =	Tla	77 n 1	Gl n	Thr	Lou
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1066 (iii) HYPOTHETICAL: NO 1067 1068 (vi) ORIGINAL SOURCE: 1069 (A) ORGANISM: Homo sapiens 1070 (H) CELL LINE: U2-OS osteosarcoma 1071 1072 (vii) IMMEDIATE SOURCE: 1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library 1074 (B) CLONE: U2-16 1075 1076 (viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153			(2, 20202)										
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1068 (vi) ORIGINAL SOURCE: 1069 (A) ORGANISM: Homo sapiens 1070 (H) CELL LINE: U2-OS osteosarcoma 1071 1072 (vii) IMMEDIATE SOURCE: 1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library 1074 (B) CLONE: U2-16 1075 1076 (viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091													
1069 (A) ORGANISM: Homo sapiens 1070 (H) CELL LINE: U2-OS osteosarcoma 1071 1072 (vii) IMMEDIATE SOURCE: 1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library 1074 (B) CLONE: U2-16 1075 1076 (viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091		(vi)	ORIGINAL S	DURCE:									
1070 1071 1072 (vii) IMMEDIATE SOURCE: 1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library 1074 (B) CLONE: U2-16 1075 1076 (viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091		(- 7			o san	iens							
1071 1072 (vii) IMMEDIATE SOURCE: 1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library 1074 (B) CLONE: U2-16 1075 1076 (viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091							sarc	oma					
1072 (vii) IMMEDIATE SOURCE: 1073			(11)										
1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library 1074 (B) CLONE: U2-16 1075 1076 (viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091		(vii)	IMMEDIATE :	SOURCE:									
1074 (B) CLONE: U2-16 1075 1076 (viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1073				S huma	an os	steo	sarc	oma	cDN2	A lib	rarv	,
1076 (viii) POSITION IN GENOME: 1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1074												
1077 (C) UNITS: bp 1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1075												
1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1076	(viii)	POSITION II	N GENOME	:								
1078 1079 (ix) FEATURE: 1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1077		(C) UNITS	: bp									
1080 (A) NAME/KEY: CDS 1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1078			_									
1081 (B) LOCATION: 6992063 1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1079	(ix)	FEATURE:										
1082 1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1080		(A) NAME/I	KEY: CDS									
1083 (ix) FEATURE: 1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1081		(B) LOCAT	ION: 699	2063	3							
1084 (A) NAME/KEY: mat_peptide 1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1082												
1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1083	(ix)	FEATURE:										
1085 (B) LOCATION: 16472060 1086 1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1084		(A) NAME/I	KEY: mat	pept	ide							
1087 (ix) FEATURE: 1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1085												
1088 (A) NAME/KEY: mRNA 1089 (B) LOCATION: 12153 1090 1091	1086												
1089 (B) LOCATION: 12153 1090 1091	1087	(ix)	FEATURE:										
1090 1091	1088		(A) NAME/I	KEY: mRN	A.								
1091	1089		(B) LOCAT	ION: 1	2153								
	1090												
1092 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	_												
	1092	(xi)	SEQUENCE D	ESCRIPTION	ON: SI	EQ II	ои с	:9:					

Raw Sequence Listing

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1093		
1094	CTGGTATATT TGTGCCTGCT GGAGGTGGAA TTAACAGTAA GAAGGAGAAA GGGATTGAAT	60
1095	ordenimi iotococci odnociodm iimanoim amadnami adoniiami	00
1096	GGACTTACAG GAAGGATTTC AAGTAAATTC AGGGAAACAC ATTTACTTGA ATAGTACAAC	120
1097	CONCILION CANCONITIC MCIMMITC ACCOMMENCE ATTINCTION AIRGINEANC	120
1098	CTAGAGTATT ATTTTACACT AAGACGACAC AAAAGATGTT AAAGTTATCA CCAAGCTGCC	180
1099	onionaliti illimator mintonato mintoniali mmalinian comaciaco	100
1100	GGACAGATAT ATATTCCAAC ACCAAGGTGC AGATCAGCAT AGATCTGTGA TTCAGAAATC	240
1101	The state of the s	210
1102	AGGATTTGTT TTGGAAAGAG CTCAAGGGTT GAGAAGAACT CAAAAGCAAG TGAAGATTAC	300
1103		300
1104	TTTGGGAACT ACAGTTTATC AGAAGATCAA CTTTTGCTAA TTCAAATACC AAAGGCCTGA	360
1105		300
1106	TTATCATAAA TTCATATAGG AATGCATAGG TCATCTGATC AAATAATATT AGCCGTCTTC	420
1107		-20
1108	TGCTACATCA ATGCAGCAAA AACTCTTAAC AACTGTGGAT AATTGGAAAT CTGAGTTTCA	480
1109		
1110	GCTTTCTTAG AAATAACTAC TCTTGACATA TTCCAAAATA TTTAAAATAG GACAGGAAAA	540
1111		0.0
1112	TCGGTGAGGA TGTTGTGCTC AGAAATGTCA CTGTCATGAA AAATAGGTAA ATTTGTTTTT	600
1113		•
1114	TCAGCTACTG GGAAACTGTA CCTCCTAGAA CCTTAGGTTT TTTTTTTTT AAGAGGACAA	660
1115		
1116	GAAGGACTAA AAATATCAAC TTTTGCTTTT GGACAAAA ATG CAT CTG ACT GTA	713
1117	Met His Leu Thr Val	
1118	-316-315	
1119		
1120	TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC TGG AGC TGC TGG GTT CTA	761
1121	Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp Ser Cys Trp Val Leu	
1122	-310 -305 -300	
1123		
1124	GTG GGT TAT GCA AAA GGA GGT TTG GGA GAC AAT CAT GTT CAC TCC AGT	809
1125	Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn His Val His Ser Ser	
1126	-295 -290 -285 -280	
1127		
1128	TTT ATT TAT AGA AGA CTA CGG AAC CAC GAA AGA CGG GAA ATA CAA AGG	857
1129	Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg Arg Glu Ile Gln Arg	
1130	-275 -270 -265	
1131		
1132	GAA ATT CTC TCT ATC TTG GGT TTG CCT CAC AGA CCC AGA CCA TTT TCA	905
1133	Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro Phe Ser	
1134	-260 -255 -250	
1135		
1136	CCT GGA AAA ATG ACC AAT CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG	953
1137	Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala Pro Leu Phe Met Leu	
1138	-245 -240 -235	
1139		
1140	GAT CTC TAC AAT GCC GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA	1001
1141	Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val	
1142	-230 -225 -220	
1143		
1144	AGG GCA TCC TTG GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA	1049

Raw Sequence Listing

04/12/93 13:28:26 S4317.raw

1145 1146	Arg Ala	Ser	Leu	Ala	Glu -21		Thr	Arg	Gly	Ala -20	_	Lys	Gly	Tyr	Pro -200	
1147	-213				-21	,				-20.	,				-200	
1148	GCC TCT	CCC	AAT	GGG	TAT	CCT	CGT	CGC	ATA	CAG	TTA	TCT	CGG	ACG	ACT	1097
1149	Ala Ser	Pro	Asn	Gly	Tyr	Pro	Arg	Arg	Ile	Gln	Leu	Ser	Arg	Thr	Thr	
1150				-19	5				-190)				-185	5	
1151																
1152	CCT CTG															1145
1153	Pro Leu	Thr			Ser	Pro	Pro			Ser	Leu	His	_		Asn	
1154			-180	0				-17	5				-170	ס		
1155 1156	mmm omo	2 2 00	(13 M	aam	a. a	3 000	ama	3 000	3.00	mmm	ama		mm s	amm.	G3.3	1100
1156	TTT CTG															1193
1158	rue neu	-16!	_	ALG	Asp	Mec	-160	_	Ser	PIIG	vaı	-155		val	GIU	
1159			•				-10	•				-15.	•			
1160	AGA GAC	AAG	GAT	TTT	TCT	CAC	CAG	CGA	AGG	CAT	TAC	AAA	GAA	TTT	CGA	1241
1161	Arg Asp															
1162	-15	_	_			-14		•			-140	_			-	
1163																
1164	TTT GAT	CTT	ACC	CAA	ATT	CCT	CAT	GGA	GAG	GCA	GTG	ACA	GCA	GCT	GAA	1289
1165	Phe Asp	Leu	Thr	Gln	Ile	Pro	His	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	
1166	-135				-130	ס				-12	5				-120	
1167																
1168	TTC CGG															1337
1169 1170	Phe Arg	TTE	Tyr	ьув -119	_	Arg	ser	Asn			Pne	GIU	Asn			
1171				-11:)				-110	,				-105	•	
1172	ATT AAG	א דידע	AGC	מדמ	тат	CAA	ATC	ATC	AAG	CAD	тас	ארא	аат	AGG	СУТ	1385
1173	Ile Lys															1505
1174			-100		-1-			-95	-1-		-1-		-90	9		
1175																
1176	GCA GAT	CTG	TTC	TTG	TTA	GAC	ACA	AGA	AAG	GCC	CAA	GCT	TTA	GAT	GTG	1433
1177	Ala Asp	Leu	Phe	Leu	Leu	Asp	Thr	Arg	Lys	Ala	Gln	Ala	Leu	Asp	Val	
1178		-85					-80					-75				
1179																
1180	GGT TGG															1481
1181	Gly Trp	Leu	vaı	Pne	Asp	_	Thr	vai	Thr	Ser		His	Trp	Val	Ile	
1182 1183	-70					-65					-60					
1184	AAT CCC	CAG	አልጥ	אממ	ጥጥር፤	GGC	тта	CAG	כידיכי	ጥርሞ	GC A	GAA	ACA	aaa	CAT	1529
1185	Asn Pro															1323
1186	-55				-50	0-7		V		-45				0 _1	-40	
1187																
1188	GGA CGC	AGT	ATC	AAC	GTA	AAA	TCT	GCT	GGT	CTT	GTG	GGA	AGA	CAG	GGA	1577
1189	Gly Arg	Ser	Ile	Asn	Val	Lys	Ser	Ala	Gly	Leu	Val	Gly	Arg	Gln	Gly	
1190				-35					-30					-25		
1191																
1192	CCT CAG															1625
1193	Pro Gln	Ser	_	Gln	Pro	Phe	Met		Ala	Phe	Phe	Lys		Ser	Glu	
1194 1105			-20					-15					-10			
1195 1196	GTA CTT	Стт	CGA	ጥሮር	ርጥር	ACA	GCA	פרר	ממ	222	CGA	222	ልልጥ	CDD	ልልሮ	1673
1190	JIA CII		CGM		G14	AUA	COA		an.		CGM		wi		-227	±0/3

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	_																
1197	Val	Leu	Leu	Arg	Ser	Val	Arg	Ala	Ala	Asn	Lys	Arg	Lys	Asn	Gln	Asn	
1198			-5					1				5					
1199																	
1200	CGC	AAT	AAA	TCC	AGC	TCT	CAT	CAG	GAC	TCC	TCC	AGA	ATG	TCC	AGT	GTT	1721
1201	Arg	Asn	Lys	Ser	Ser	Ser	His	Gln	Asp	Ser	Ser	Arg	Met	Ser	Ser	Val	
1202	10					15					20					25	
1203																	
1204	GGA	GAT	TAT	AAC	ACA	AGT	GAG	CAA	AAA	CAA	GCC	TGT	AAG	AAG	CAC	GAA	1769
1205	Gly	Asp	Tyr	Asn	Thr	Ser	Glu	Gln	Lys	Gln	Ala	Сув	Lys	Lys	His	Glu	
1206	_	_	-		30				-	35		-	-	-	40		
1207																	
1208	CTC	TAT	GTG	AGC	TTC	CGG	GAT	CTG	GGA	TGG	CAG	GAC	TGG	ATT	ATA	GCA	1817
1209					Phe												
1210		-4-		45		3			50					55			
1211																	
1212	CCA	GAA	GGA	TAC	GCT	GCA	ጥጥጥ	ТАТ	тст	GAT	GGA	GAA	тст	тст	ттт	CCA	1865
1213					Ala												1003
1214	1.0	GIU	60	- 7 -	ALG	AIG	1110	65	Cys	rop	GLY	GIU	70	Der	r 116	FIO	
1215			00					05					, 0				
1216	Comm	220	ccc	CAT	ATG	3 3 T	CCC	N.C.C	220	CAC	CCM	አጥአ	CITITO	CNC	N CIT	CTC	1913
1217																	1913
1217	Tea		ATA	urs	Met	ABII		Inr	ASII	нтв	ATA		var	GIN	Thr	rea	
		75					80					85					
1219	amm	~~ m	ama.	3 ma	mmm	~~	~~	~~	am.	-		~~			aam	aa 3	1001
1220					TTT												1961
1221		HIS	Leu	Met	Phe		Asp	HIS	vaı	Pro		Pro	сув	Cys	АТа		
1222	90					95					100					105	
1223																	
1224					GCC												2009
1225	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu		Phe	Asp	Asp	Ser		Asn	
1226					110					115					120		
1227																	
1228					AAA												2057
1229	Val	Ile	Leu	-	Lys	Tyr	Arg	Asn		Val	Val	Arg	Ser		Gly	Cys	
1230				125					130					135			
1231																	
1232	_	TAA:	CATT	AAA :	TAAT	ATTG/	AT A	ATAA(CAAA	A AG	ATCT	STAT	TAAC	GTT:	ΓAΤ		2110
1233	His																
1234																	
1235																	
1236	GGC:	rgca.	ATA A	AAAA(SCAT	AC T	rtca(BACA	A AC	AGAA	AAAA	AAA					2153
1237																	
1238																	
1239	(2)	INF	DRMA'	CION	FOR	SEQ	ID 1	10:10	0:								
1240																	
1241			(i) S	SEQUI	ENCE	CHAI	RACTI	ERIS:	rics:	:							
1242					LEN					acida	3						
1243				(B)	TYI	PE: 8	amino	ac	id								
1244				(D)	TOI	OLO	GY:]	linea	ar								
1245																	
1246		(:	Li) 1	MOLE	CULE	TYPI	E: pi	rote:	in								
1247																	
1248		(3	ci) S	SEQUI	ENCE	DESC	CRIP	CION	: SE	QI Ç	NO:	LO:					

Raw Sequence Listing

04/12/93 13:28:39 S4317.raw

1249 1250 1251 1252	Met His Leu -316 -315	Thr Val	Phe Leu Leu -310	Lys Gly Ile	Val Gly Ph	e Leu Trp
1253 1254 1255	Ser Cys Trp -300	Val Leu	Val Gly Tyr -295	Ala Lys Gly	Gly Leu Gl 290	y Asp Asn -285
1256 1257 1258	His Val His	Ser Ser -280	_	Arg Arg Leu -275	ı Arg Asn Hi	s Glu Arg -270
1259 1260 1261	Arg Glu Ile	Gln Arg	Glu Ile Leu	Ser Ile Leu -260	Gly Leu Pr	o His Arg -255
1262 1263 1264	Pro Arg Pro			Met Thr Asr 45	Gln Ala Se -240	
1265 1266 1267	Pro Leu Phe -235	Met Leu	Asp Leu Tyr -230	Asn Ala Glu	Glu Asn Pr -225	o Glu Glu
1268 1269 1270	Ser Glu Tyr -220	Ser Val	Arg Ala Ser -215	Leu Ala Glu	Glu Thr Ar 210	g Gly Ala -205
1271 1272 1273	Arg Lys Gly	Tyr Pro -200		Asn Gly Tyr -195	Pro Arg Ar	g Ile Gln -190
1274 1275 1276	Leu Ser Arg	Thr Thr	Pro Leu Thr	Thr Gln Ser	Pro Pro Le	eu Ala Ser -175
1277 1278 1279	Leu His Asp -17			Asp Ala Asp 65	Met Val Me -160	
1280 1281 1282	Val Asn Leu -155	. Val Glu	Arg Asp Lys -150	Asp Phe Ser	His Gln Ar -145	g Arg His
1283 1284 1285	Tyr Lys Glu -140	Phe Arg	Phe Asp Leu -135	Thr Gln Ile	Pro His Gl	y Glu Ala -125
1286 1287 1288	Val Thr Ala	Ala Glu -120	_	Tyr Lys Asp -115	Arg Ser As	n Asn Arg -110
1289 1290 1291	Phe Glu Asn	Glu Thr	Ile Lys Ile	Ser Ile Tyr -100	Gln Ile Il	e Lys Glu -95
1292 1293	Tyr Thr Asn		Ala Asp Leu -85	Phe Leu Leu	Asp Thr Ar	g Lys Ala
1294	-90		-03			
1294 1295 1296 1297				. Val Phe Asp		al Thr Ser

Raw Sequence Listing

04/12/93 13:28:46 S4317.raw

1301 1302 1303	Ala	Glu	Thr	Gly	Asp -40	Gly	Arg	Ser	Ile	Asn -35	Val	Lys	Ser	Ala	Gly -30	Leu
1304 1305 1306	Val	Gly	Arg	Gln -25	Gly	Pro	Gln	Ser	Lys -20	Gln	Pro	Phe	Met	Val -15	Ala	Phe
1307 1308 1309	Phe	Lys	Ala -10	Ser	Glu	Val	Leu	Leu -5	Arg	Ser	Val	Arg	Ala 1	Ala	Asn	Lys
1310 1311 1312	Arg 5	Lys	Asn	Gln	Asn	Arg 10	Asn	Lys	Ser	Ser	Ser 15	His	Gln	Asp	Ser	Ser 20
1313 1314 1315	Arg	Met	Ser	Ser	Val 25	Gly	Asp	Tyr	Asn	Thr 30	Ser	Glu	Gln	Lys	Gln 35	Ala
1316 1317 1318	Сув	Lys	Lys	His 40	Glu	Leu	Tyr	Val	Ser 45	Phe	Arg	Asp	Leu	Gly 50	Trp	Gln
1319 1320 1321	Asp	Trp	Ile 55	Ile	Ala	Pro	Glu	Gly 60	Tyr	Ala	Ala	Phe	Tyr 65	Сув	Asp	Gly
1322 1323 1324	Glu	Сув 70	Ser	Phe	Pro	Leu	Asn 75	Ala	His	Met	Asn	Ala 80	Thr	Asn	His	Ala
1325 1326 1327	Ile 85	Val	Gln	Thr	Leu	Val 90	His	Leu	Met	Phe	Pro 95	Asp	His	Val	Pro	Lys 100
1328 1329 1330	Pro	Сув	Сув	Ala	Pro 105	Thr	Lys	Leu	Asn	Ala 110	Ile	Ser	Val	Leu	Tyr 115	Phe
1331 1332 1333	Asp	Asp	Ser	Ser 120	Asn	Val	Ile	Leu	Lys 125	Lys	Tyr	Arg	Asn	Met 130	Val	Val
1334 1335 1336	Arg	Ser	Cys 135	Gly	Сув	His										
1337 1338 1339	(2)	INF	ORMA	rion	FOR	SEQ	ID 1	10:1	L:							
1340 1341		(i)	(2	À) LI	CE CI ENGTI	I: 10	003 l	oase	pair	rs						
1342 1343 1344			((c) s:	PE: TRANI OPOLO	DEDNI	SS:	doub	ole							
1345 1346 1347		(ii)	MOI	LECUI	LE T	PE:	CDN	A to	mRN	A.						
1348 1349 1350		(iii)														
1351 1352		(V1)	(2	4) OI	AL SO RGAN: ESSUI	ESM:	Homo									

Raw Sequence Listing

04/12/93 13:28:53 S4317.raw

1353														
1354	(vii)	IMMEDI												
1355		(A) L	IBRAR	Y: Hu	nan he	art	cDNA	lib	cary	str	atage	ene (catalog	
1356			#93	6208										
1357		(B) C	LONE:	hH38										
1358														
1359	(viii)	POSITI	ON IN	GENO	Œ:									
1360		(C) U	NITS:	bр										
1361														
1362	(ix)	FEATUR	E:											
1363		(A) N	AME/K	EY: CI	S									
1364		(B) L	OCATI	ON: 8	.850									
1365														
1366	(ix)	FEATUR	E:											
1367		(A) N	AME/K	EY: ma	it pep	tide								
1368		(B) L	OCATI	ON: 42	2784	3								
1369														
1370	(ix)	FEATUR	E:											
1371		(A) N	AME/K	EY: ml	ANS									
1372				ON: 1										
1373														
1374														
1375	(xi)	SEQUEN	CE DE	SCRIP:	: NOI:	SEQ	ID NO	:11	;					
1376		_				-								
1377	GAATTCC	GAG CCC	CAT	TGG A	G GAG	TTC	CGC	TTT	GAC	CTG	ACC	CAG	ATC	49
1378		Glu Pro	His	Trp Ly	s Glu	Phe	Arg	Phe	Asp	Leu	Thr	Gln	Ile	
1379		-139			L35				-130	כ				
1379 1380									-130	ס				
1380	CCG GCT	-139	GCG	-:	L 3 5	GCG	GAG	TTC			TAC	AAG	GTG	97
1380 1381	CCG GCT	-139 GGG GAG		GTC A	.35 CA GCT				CGG	ATT				97
1380 1381 1382	Pro Ala	-139 GGG GAG		GTC AC	.35 CA GCT			Phe	CGG Arg	ATT			Val	97
1380 1381 1382 1383		-139 GGG GAG		GTC A	.35 CA GCT				CGG Arg	ATT				97
1380 1381 1382 1383 1384	Pro Ala -125	-139 GGG GAG Gly Glu	Ala	GTC AC Val TI -120	l35 CA GCT ir Ala	Ala	Glu	Phe -11	CGG Arg	ATT Ile	Tyr	Lys	Val -110	
1380 1381 1382 1383 1384 1385	Pro Ala -125 CCC AGC	-139 GGG GAG Gly Glu ATC CAC	Ala	GTC AC Val Tl -120	.35 CA GCT or Ala	Ala	Glu	Phe -115	CGG Arg	ATT Ile	Tyr	Lys	Val -110 CAG	97 145
1380 1381 1382 1383 1384 1385 1386	Pro Ala -125	-139 GGG GAG Gly Glu ATC CAC	Ala CTG Leu	GTC AG Val Tl -120 CTC AJ Leu As	.35 CA GCT or Ala	Ala	Glu CTC Leu	Phe -11! CAC His	CGG Arg	ATT Ile	Tyr	Lys TTC Phe	Val -110 CAG	
1380 1381 1382 1383 1384 1385 1386 1387	Pro Ala -125 CCC AGC	-139 GGG GAG Gly Glu ATC CAC	Ala	GTC AG Val Tl -120 CTC AJ Leu As	.35 CA GCT or Ala	Ala	Glu	Phe -11! CAC His	CGG Arg	ATT Ile	Tyr	Lys	Val -110 CAG	
1380 1381 1382 1383 1384 1385 1386 1387 1388	Pro Ala -125 CCC AGC Pro Ser	-139 GGG GAG Gly Glu ATC CAC Ile His	CTG Leu -105	GTC AC Val Tl -120 CTC AL Leu As	A GCT TALA AC AGG	Ala ACC Thr	CTC Leu	Phe -115 CAC His	CGG Arg GTC Val	ATT Ile AGC Ser	Tyr ATG Met	TTC Phe -95	Val -110 CAG Gln	145
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389	Pro Ala -125 CCC AGC Pro Ser	GGG GAGGLY GLU ATC CACILE His	CTG Leu -105	GTC AC Val TI -120 CTC AL Leu As	CA GCT TALA AC AGG EN ATG	Ala ACC Thr	Glu CTC Leu -100	Phe -115 CAC His	CGG Arg GTC Val	ATT Ile AGC Ser	Tyr ATG Met	TTC Phe -95	Val -110 CAG Gln	
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390	Pro Ala -125 CCC AGC Pro Ser	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu	CTG Leu -105 CAG	GTC AC Val TI -120 CTC AL Leu As	CA GCT TALA AC AGG EN ATG	Ala ACC Thr GAG Glu	Glu CTC Leu -100	Phe -115 CAC His	CGG Arg GTC Val	ATT Ile AGC Ser	Tyr ATG Met	TTC Phe -95	Val -110 CAG Gln	145
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391	Pro Ala -125 CCC AGC Pro Ser	GGG GAGGLY GLU ATC CACILE His	CTG Leu -105 CAG	GTC AC Val TI -120 CTC AL Leu As	CA GCT TALA AC AGG EN ATG	Ala ACC Thr	Glu CTC Leu -100	Phe -115 CAC His	CGG Arg GTC Val	ATT Ile AGC Ser	Tyr ATG Met	TTC Phe -95	Val -110 CAG Gln	145
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu	CTG Leu -105 CAG	GTC AC Val Tl -120 CTC AL Leu As	CA GCT or Ala AC AGG on Arg AC AGG	Ala ACC Thr GAG Glu -85	Glu CTC Leu -100 TCT Ser	Phe -11! CAC His) GAC Asp	CGG Arg GTC Val TTG Leu	ATT Ile AGC Ser TTC Phe	Tyr ATG Met TTT Phe -80	TTC Phe -95 TTG Leu	Val -110 CAG Gln GAT Asp	145 193
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90	CTG Leu -105 CAG Gln	GTC AC Val TI -120 CTC AL Leu As TCC AL Ser As	CA GCT or Ala AC AGG an Arg AC AGG an Arg	Ala ACC Thr GAG Glu -85	Glu CTC Leu -100 TCT Ser	Phe -11! CAC His CAC Asp	CGG Arg GTC Val TTG Leu	ATT Ile AGC Ser TTC Phe	Tyr ATG Met TTT Phe -80 CTG	TTC Phe -95 TTG Leu	Val -110 CAG Gln GAT Asp	145
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu	CTG Leu -105 CAG Gln	GTC AC Val TI -120 CTC AL Leu As TCC AL Ser As	CA GCT TALA CC AGG TALC ACC	Ala ACC Thr GAG Glu -85	Glu CTC Leu -100 TCT Ser	Phe -11! CAC His CAC Asp	CGG Arg GTC Val TTG Leu	ATT Ile AGC Ser TTC Phe GTG Val	Tyr ATG Met TTT Phe -80 CTG	TTC Phe -95 TTG Leu	Val -110 CAG Gln GAT Asp	145 193
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90	CTG Leu -105 CAG Gln	GTC AC Val TI -120 CTC AL Leu As TCC AL Ser As	CA GCT or Ala AC AGG an Arg AC AGG an Arg	Ala ACC Thr GAG Glu -85	Glu CTC Leu -100 TCT Ser	Phe -11! CAC His CAC Asp	CGG Arg GTC Val TTG Leu	ATT Ile AGC Ser TTC Phe	Tyr ATG Met TTT Phe -80 CTG	TTC Phe -95 TTG Leu	Val -110 CAG Gln GAT Asp	145 193
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG Leu Gln	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu -75	CTG Leu -105 CAG Gln	GTC AC Val Tl -120 CTC AL Leu As TCC AL Ser As	CA GCT TALA AC AGG ATG	Ala ACC Thr GAG Glu -85 GAG Glu	Glu CTC Leu -100 TCT Ser GGC Gly	Phe -115 CAC His GAC Asp	CGG Arg GTC Val TTG Leu CTG	ATT Ile AGC Ser TTC Phe GTG Val -65	Tyr ATG Met TTT Phe -80 CTG Leu	TTC Phe -95 TTG Leu GAT Asp	Val -110 CAG Gln GAT Asp GTC Val	145 193 241
1380 1381 1382 1383 1384 1385 1386 1387 1388 1399 1390 1391 1392 1393 1394 1395 1396 1397	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG Leu Gln ACA GCA	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu -75 GCC AGT	CTG Leu -105 CAG Gln CGA	GTC AC Val Tl -120 CTC AL Leu As TCC AL Ser As GCT GC Al GCT GC TCC TCC TCC TCC TCC TCC TCC TCC	CA GCT TALA CA AGG ATG AC AGG ATG AC AGG ATG AC AGG TTG	Ala ACC Thr GAG Glu -85 GAG Glu CTG	Glu CTC Leu -100 TCT Ser GGC Gly	Phe -115 CAC His GAC Asp TGG Trp	CGG Arg GTC Val TTG Leu CTG Leu	ATT Ile AGC Ser TTC Phe GTG Val -65	Tyr ATG Met TTT Phe -80 CTG Leu GAC	TTC Phe -95 TTG Leu GAT Asp	Val -110 CAG Gln GAT Asp GTC Val	145 193
1380 1381 1382 1383 1384 1385 1386 1387 1388 1399 1390 1391 1392 1393 1394 1395 1396 1397 1398	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG Leu Gln ACA GCA Thr Ala	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu -75 GCC AGT	CTG Leu -105 CAG Gln CGA	GTC AC Val Tl -120 CTC AL Leu As TCC AL Ser As GCT GC AL GCT GC AL GCT GC TC AL GCT GC TC AL GCT	CA GCT TALA CAGG ACAGG	Ala ACC Thr GAG Glu -85 GAG Glu CTG	Glu CTC Leu -100 TCT Ser GGC Gly	Phe -115 CAC His GAC Asp TGG Trp	CGG Arg GTC Val TTG Leu CTG Leu	ATT Ile AGC Ser TTC Phe GTG Val -65	Tyr ATG Met TTT Phe -80 CTG Leu GAC	TTC Phe -95 TTG Leu GAT Asp	Val -110 CAG Gln GAT Asp GTC Val	145 193 241
1380 1381 1382 1383 1384 1385 1386 1387 1388 1399 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG Leu Gln ACA GCA	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu -75 GCC AGT	CTG Leu -105 CAG Gln CGA	GTC AC Val Tl -120 CTC AL Leu As TCC AL Ser As GCT GC AL GCT GC AL GCT GC TC AL GCT GC TC AL GCT	CA GCT TALA CA AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG	Ala ACC Thr GAG Glu -85 GAG Glu CTG	Glu CTC Leu -100 TCT Ser GGC Gly	Phe -115 CAC His GAC Asp TGG Trp	CGG Arg GTC Val TTG Leu CTG Leu	ATT Ile AGC Ser TTC Phe GTG Val -65	Tyr ATG Met TTT Phe -80 CTG Leu GAC	TTC Phe -95 TTG Leu GAT Asp	Val -110 CAG Gln GAT Asp GTC Val	145 193 241
1380 1381 1382 1383 1384 1385 1386 1387 1388 1399 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG Leu Gln ACA GCA Thr Ala -60	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu -75 GCC AGT Ala Ser	CTG Leu -105 CAG GIn CGA Arg	GTC AC Val Tl -120 CTC AL Leu As TCC AL Ser As GCT GC AC	CA GCT TALA CAGG TAGA CAGG ACAGG ACAGG ACAGG TTG TTG TTG TTG	Ala ACC Thr GAG Glu -85 GAG Glu CTG Leu	Glu CTC Leu -100 TCT Ser GGC Gly AAG Lys	Phe -115 CAC His GAC Asp TGG Trp	CGG Arg GTC Val TTG Leu CTG Leu CAC His	ATT Ile AGC Ser TTC Phe GTG Val -65 AAG Lys	Tyr ATG Met TTT Phe -80 CTG Leu GAC Asp	TTC Phe -95 TTG Leu GAT Asp	Val -110 CAG Gln GAT Asp GTC Val GGA Gly	145 193 241 289
1380 1381 1382 1383 1384 1385 1386 1387 1388 1399 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG Leu Gln ACA GCA Thr Ala -60 CTC CGC	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu -75 GCC AGT Ala Ser	CTG Leu -105 CAG Gln CGA Arg GAC Asp	GTC AC Val Tl -120 CTC AL Leu As TCC AL Ser As GCT GC TC CYS T: -!	CA GCT Ala AC AGG AT ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG AC	Ala ACC Thr GAG Glu -85 GAG Glu CTG Leu GAT	Glu CTC Leu -100 TCT Ser GGC Gly AAG Lys	Phe -115 CAC His GAC Asp TGG Trp CGT Arg	CGG Arg GTC Val TTG Leu CTG Leu CAC His -50	ATT Ile AGC Ser TTC Phe GTG Val -65 AAG Lys	TYT ATG Met TTT Phe -80 CTG Leu GAC Asp	Lys TTC Phe -95 TTG Leu GAT Asp CTG Leu CCT	Val -110 CAG Gln GAT Asp GTC Val GGA Gly	145 193 241
1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG Leu Gln ACA GCA Thr Ala -60 CTC CGC Leu Arg	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu -75 GCC AGT Ala Ser	CTG Leu -105 CAG GIn CGA Arg GAC Asp	GTC AC Val Ti -120 CTC AL Leu A. TCC AL Ser A. GCT GC TC Cys T.	CA GCT Ala AC AGG AT ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG AC	Ala ACC Thr GAG Glu -85 GAG Glu CTG Leu GAT	Glu CTC Leu -100 TCT Ser GGC Gly AAG Lys	Phe -11! CAC His GAC Asp TGG Trp CGT Arg	CGG Arg GTC Val TTG Leu CTG Leu CAC His -50	ATT Ile AGC Ser TTC Phe GTG Val -65 AAG Lys	TYT ATG Met TTT Phe -80 CTG Leu GAC Asp	Lys TTC Phe -95 TTG Leu GAT Asp CTG Leu CCT	Val -110 CAG Gln GAT Asp GTC Val GGA Gly GGC Gly	145 193 241 289
1380 1381 1382 1383 1384 1385 1386 1387 1388 1399 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401	Pro Ala -125 CCC AGC Pro Ser GTG GTC Val Val CTT CAG Leu Gln ACA GCA Thr Ala -60 CTC CGC	GGG GAG Gly Glu ATC CAC Ile His CAG GAG Gln Glu -90 ACG CTC Thr Leu -75 GCC AGT Ala Ser	CTG Leu -105 CAG GIn CGA Arg GAC Asp	GTC AC Val Tl -120 CTC AL Leu As TCC AL Ser As GCT GC TC CYS T: -!	CA GCT Ala AC AGG AT ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG ATG AC AGG AC	Ala ACC Thr GAG Glu -85 GAG Glu CTG Leu GAT	Glu CTC Leu -100 TCT Ser GGC Gly AAG Lys	Phe -115 CAC His GAC Asp TGG Trp CGT Arg	CGG Arg GTC Val TTG Leu CTG Leu CAC His -50	ATT Ile AGC Ser TTC Phe GTG Val -65 AAG Lys	TYT ATG Met TTT Phe -80 CTG Leu GAC Asp	Lys TTC Phe -95 TTG Leu GAT Asp CTG Leu CCT	Val -110 CAG Gln GAT Asp GTC Val GGA Gly	145 193 241 289

Raw Sequence Listing

04/12/93 13:29:00 S4317.raw

1405															CCT		385
1406	Leu	Ala	Gly	Leu	Leu	Gly	Gln	Arg	Ala	Pro	Arg	Ser	Gln	Gln	Pro	Phe	
1407					-25					-20					-15		
1408																	
1409	GTG	GTC	ACT	TTC	TTC	AGG	GCC	AGT	CCG	AGT	CCC	ATC	CGC	ACC	CCT	CGG	433
1410	Val	Val	Thr	Phe	Phe	Arg	Ala	Ser	Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg	
1411				-10					-5				_	1		_	
1412																	
1413	GCA	GTG	AGG	CCA	CTG	AGG	AGG	AGG	CAG	CCG	AAG	AAA	AGC	AAC	GAG	CTG	481
1414			_												Glu		
1415		5					10	3			-4 -	15					
1416		_															
1417	CCG	CAG	GCC	AAC	CGA	CTC	CCA	GGG	ATC	ጥጥጥ	GAT	GAC	GTC	CAC	GGC	TCC	529
1418															Gly		323
1419	20	01	nia	AGII	n-9	25	110	GLY	**6	1110	30	voñ	407	1110	GIY	35	
1420	20					23					30					33	
1421	CAC	cac	caa	CAC	CTC	TOO	CCT	000	CA C	as a	CITIC	ma a	CTC	3.00	TTC	C A C	E77
1422																	577
1422	uis	СТУ	Arg	GIII		Сув	Arg	Arg	HIS		Leu	ıyr	val	ser	Phe	GIN	
-					40					45					50		
1424	a. a	~~~	~~~					~~~		~~~	~~~	~- -	~~~				
1425															TCA		625
1426	Asp	Leu	GIY		Leu	Asp	rrp	val		Ala	Pro	GIn	GIY	-	Ser	Ala	
1427				55					60					65			
1428																	
1429															ATG		673
1430	Tyr	Tyr	_	Glu	Gly	Glu	Сув	Ser	Phe	Pro	Leu	Asp	Ser	Сув	Met	Asn	
1431			70					75					80				
1432																	
1433	GCC	ACC	AAC	CAC	GCC	ATC	CTG	CAG	TCC	CTG	GTG	CAC	CTG	ATG	AAG	CCA	721
1434	Ala	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	
1435		85					90					95					
1436																	
1437	AAC	GCA	GTC	CCC	AAG	GCG	TGC	TGT	GCA	CCC	ACC	AAG	CTG	AGC	GCC	ACC	769
1438	Asn	Ala	Val	Pro	Lys	Ala	Сув	Cys	Ala	Pro	Thr	Lys	Leu	Ser	Ala	Thr	
1439	100					105					110	-				115	
1440																	
1441	TCT	GTG	CTC	TAC	TAT	GAC	AGC	AGC	AAC	AAC	GTC	ATC	CTG	CGC	AAG	CAC	817
1442	Ser	Val	Leu	Tyr	Tyr	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg	Lys	His	
1443				-	120	_				125				_	130		
1444																	
	CGC	AAC	ATG	GTG	GTC	AAG	GCC	TGC	GGC	TGC	CAC	TGAC	STCA	3CC (CGCC	CAGCCC	870
1446				Val													
1447				135		_4 -		- 4 -	140	- 4 -							
1448																	
1449	TACT	CGCAC	CC 2	ACCCI	TCTC	CA TO	TGG	ATCG	g GCC	CCTGC	CAGA	GGC	AGAA	AAC (CCTT	AATGC	930
1450					,												
1451	тстс	יאכיאנ	CT C	BAGG	ZAGGZ	ል G ጥ	TCAC	3666	ם ככי	rcac'i	гстс	GGT	CCT	ACT '	rccro	STCAGG	990
1452	-51					\											220
1453	CTTC	тее	BAA 1	רידיכי													1003
1454																	
1455																	
	(2)	TNW	ימאקר	יד הא	MUD.	SEO	י חד	ر. ۱۰ مه	2 •								
7.430	(4)	TME	ALTH.	TON	FUR	SPC	ועב	40 i 14									

Raw Sequence Listing

04/12/93 13:29:06 S4317.raw

1457																
1458			(i) :													
1459						NGTH				acid	3					
1460						PE: a										
1461				(D)	TO:	POLO	GY:	line	ar							
1462																
1463		(:	ii) 1	MOLE	CULE	TYPI	E: p:	rote:	in							
1464																
1465		(:	ki) :	SEQUI	ence	DES	CRIP'	rion	: SE(D ID	NO:	12:				
1466																
1467			His	\mathtt{Trp}			Phe	Arg	Phe	Asp	Leu	Thr	Gln	Ile	Pro	Ala
1468	-13	9			-13	35				-:	130					-125
1469																
1470	Gly	Glu	Ala			Ala	Ala	Glu			Ile	Tyr	Lys			Ser
1471				-12	כ				-13	15				-:	110	
1472																
1473	Ile	His	Leu		Asn	Arg	Thr			Val	Ser	Met			Val	Val
1474			-10	5				-10	00				- 9	95		
1475		=		_	_	_	-	_	_	_		_				_
1476	Gln		Gln	Ser	Asn	Arg		Ser	Asp	Leu	Phe		Leu	Asp	Leu	Gln
1477		-90					-85					-80				
1478		_	_			_			_	_		_	_			
1479		Leu	Arg	Ala	GTÄ	_	Glu	Gly	Trp	Leu		Leu	Asp	Val	Thr	
1480	-75					-70					-65					-60
1481			•	~		. .			_		_	_	_		_	_
1482	Ala	ser	Asp	Сув	_	ьeu	Leu	ьyв	Arg		гув	Asp	Leu	GIA		Arg
1483					-55					-50					-45	
1484 1485	T	M	77.7	a1	m1	a1	3	~1	TT -	a	777	3	D	~ 1	.	
1485	ьeu	Tyr	Val	-40	Thr	GIU	Asp	GIĀ		ser	vaı	Asp	Pro	_	ьеи	Ala
1487				-40					-35					-30		
1488	Clv.	T.011	Leu	Gl v	Gln.	2	212	Dro	7~~	gor.	Gl n	Gl n	Dro	Dho	37-1	17-1
1489	GLY	пец	-25	GLY	GIII	ALG	ALG	-20	Arg	per	GIII	GIII	-15	FIIG	vai	Val
1490			-25					-20					-15			
1491	Thr	Phe	Phe	Ara	Δla	Ser	Pro	Ser	Pro	Tla	Δτα	Thr	Dro	Ara	Δla	Val
1492		-10		9	****	501	-5	501	110	110	9	1	110	nr 9	n.u	5
1493												-				,
1494	Ara	Pro	Leu	Arα	Ara	Ara	Gln	Pro	ī.vs	Lvs	Ser	Agn	Glu	T.e.11	Pro	Gln
1495	9			9	10	9	V		-,,,	15	-	****	014		20	
1496																
1497	Ala	Asn	Ara	Leu	Pro	Glv	Ile	Phe	asp	Asp	Val	His	Glv	Ser	His	Gly
1498			3	25		2			30				1	35		2
1499																
1500	Ara	Gln	Val	Сув	Ara	Ara	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	asA	Leu
1501	-		40	_	- 3			45		_			50		- 6	-
1502																
1503	Gly	Trp	Leu	Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	Tyr	Tyr
1504	•	55		-	_		60				-	65			-	_
1505																
1506	Cys	Glu	Gly	Glu	Cys	Ser	Phe	Pro	Leu	qaA	Ser	Сув	Met	Asn	Ala	Thr
1507	70					75					80					85
1508																

Raw Sequence Listing

04/12/93 13:29:13 S4317.raw

1509	Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala	
1510	90 95 100	
1511		
1512	Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val	
1513	105 110 115	
1514		
1515	Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn	
1516	120 125 130	
1517		
1518	Met Val Val Lys Ala Cys Gly Cys His	
1519	135 140	
1520		
1521	(2) INFORMATION FOR SEQ ID NO:13:	
1522		
1523	(i) SEQUENCE CHARACTERISTICS:	
1524	(A) LENGTH: 3623 base pairs	
1525	(B) TYPE: nucleic acid	
1526	(C) STRANDEDNESS: double	
1527	(D) TOPOLOGY: linear	
1528		
1529	(ii) MOLECULE TYPE: DNA	
1530		
1531		
1532	(vii) IMMEDIATE SOURCE:	
1533	(B) CLONE: pALBP2-781	
1534		
1535	(ix) FEATURE:	
1536	(A) NAME/KEY: CDS	
1537	(B) LOCATION: 27243071	
1538		
1539	(ix) FEATURE:	
1540	(A) NAME/KEY: terminator	
1541	(B) LOCATION: 31503218	
1542		
1543	(ix) FEATURE:	
1544	(A) NAME/KEY: RBS	
1545	(B) LOCATION: 22222723	
1546		
1547		
1548	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
1549		
1550	GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT	60
1551		
1552	CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT 1	20
1553		
1554	PCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT 1	80
1555		
1556	ANTATTGANA ANGGANGAGT ATGAGTATTC ANCATTTCCG TGTCGCCCTT ATTCCCTTTT 2	40
1557		
1558	TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 3	00
1559	AMALIALAN ARRAGARAN ASIARARAN NANTANIAN ARRAGARAN NANTANIAN ARRAGARAN NANTANIAN ARRAGARAN NANTANIAN ARRAGARAN	
1560	CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA 3	60

Raw Sequence Listing

04/12/93 13:29:20 S4317.raw

1561 1562	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	ТТССА АТСАТ	CACCACTTT T	እ እ እ ርጥጥርጥር	420
1563	100110110110	111100000	OILLOILLOI I	IICCMIONI	ONGCACIIII	AMGIICIGC	120
1564	TATGTGGCGC	GGTATTATCC	CGTATTGACG	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	480
1565							
1566	ACTATTCTCA	GAATGACTTG	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	540
1567 1568	GGN MGN GN GM	33 <i>G</i> 3 <i>G</i> 33 <i>m</i> m3	maas amaama	GG1 M1 1 GG1 M	a. a. a. a. a. a.	1 CTCCCCCC	600
1569	GCATGACAGT	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	600
1570	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	CACAACATGG	660
1571							
1572	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	GAATGAAGCC	ATACCAAACG	720
1573							
1574	ACGAGCGTGA	CACCACGATG	CCTGTAGCAA	TGGCAACAAC	GTTGCGCAAA	CTATTAACTG	780
1575 1576	ሮሮሮል እርሞእርሞ	TACTCTAGCT	TCCCCCCA A C	33TT33T3C3	CTCC A TCC A C	CCCCAMAAAC	840
1577	GCGAACIACI	IACICIAGCI	TCCCGGCAAC	AATTAATAGA	CIGGAIGGAG	GCGGATAAAG	040
1578	TTGCAGGACC	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	900
1579							
1580	GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	GGTAAGCCCT	960
1581							
1582	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	TATGGATGAA	CGAAATAGAC	1020
1583 1584	A CA TCCCTCA	GATAGGTGCC	ጥሮ እ ሮጥር እ ጥጥ እ	እ <i>ርር</i> እጥጥርርጥ እ	3 CTCTC3 C3 C	C3 3 CTTT 3 CT	1080
1585	AGAICGCIGA	GATAGGTGCC	ICACIGATIA	AGCATIGGIA	ACIGICAGAC	CAAGIIIACI	1080
1586	CATATATACT	TTAGATTGAT	TTAAAACTTC	ATTTTTAATT	TAAAAGGATC	TAGGTGAAGA	1140
1587							
1588	TCCTTTTTGA	TAATCTCATG	ACCAAAATCC	CTTAACGTGA	GTTTTCGTTC	CACTGAGCGT	1200
1589							
1590 1591	CAGACCCCGT	AGAAAAGATC	AAAGGATCTT	CTTGAGATCC	TTTTTTTCTG	CGCGTAATCT	1260
1592	GCTGCTTGCA	AACAAAAAA	CCACCGCTAC	СУССССТССТ	ттстттсссс	GATCAAGAGC	1320
1593				3		0	2320
1594	TACCAACTCT	TTTTCCGAAG	GTAACTGGCT	TCAGCAGAGC	GCAGATACCA	AATACTGTCC	1380
1595							
1596	TTCTAGTGTA	GCCGTAGTTA	GGCCACCACT	TCAAGAACTC	TGTAGCACCG	CCTACATACC	1440
1597 1598	TO COTOTO COT	3 3 m///m//mm3	CCACTCCCTC	CTCCCA CTCC	CCAMAACTICC	mamamma aaa	1500
1599	ICGCICIGCI	AATCCTGTTA	CCAGIGGCIG	CIGCCAGIGG	CGATAAGTCG	TGTCTTACCG	1500
1600	GGTTGGACTC	AAGACGATAG	TTACCGGATA	AGGCGCAGCG	GTCGGGCTGA	ACGGGGGGTT	1560
1601							
1602	CGTGCACACA	GCCCAGCTTG	GAGCGAACGA	CCTACACCGA	ACTGAGATAC	CTACAGCGTG	1620
1603							
1604	AGCATTGAGA	AAGCGCCACG	CTTCCCGAAG	GGAGAAAGGC	GGACAGGTAT	CCGGTAAGCG	1680
1605 1606	GCAGGGTCGG	AACAGGAGAG	CGCACGAGGG	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT	1740
1607	3		Jourounded		Journa	LOUINICITI	1/40
1608	ATAGTCCTGT	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA	TGCTCGTCAG	1800
1609							
1610	GGGGGCGGAG	CCTATGGAAA	AACGCCAGCA	ACGCGGCCTT	TTTACGGTTC	CTGGCCTTTT	1860
1611 1612	CCTCCCCCTTTT	mccmas as ma	mmammaama	CCDD D DCCCC	ma a mmamama	CAMA ACCOMS	1000
1012	GCTGGCCTTT	IGCICACATG	TICTITCCTG	CGITATCCCC	IGALICIGIG	GATAACCGTA	1920

Raw Sequence Listing

04/12/93 13:29:27 S4317.raw

1613 1614	MM1.000.00MM	1000
1615	TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT	1980
1616	CAGTGAGCGA GGAAGCGGAA GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC	2040
1617		2010
1618	CGATTCATTA ATGCAGAATT GATCTCTCAC CTACCAAACA ATGCCCCCCT GCAAAAAATA	2100
1619		
1620	AATTCATATA AAAAACATAC AGATAACCAT CTGCGGTGAT AAATTATCTC TGGCGGTGTT	2160
1621		
1622	GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GGACGCACTG ACCACCATGA	2220
1623		
1624	AGGTGACGCT CTTAAAAATT AAGCCCTGAA GAAGGGCAGC ATTCAAAGCA GAAGGCTTTG	2280
1625		
1626 1627	GGGTGTGTGA TACGAAACGA AGCATTGGCC GTAAGTGCGA TTCCGGATTA GCTGCCAATG	2340
1627	TGCCAATCGC GGGGGGTTTT CGTTCAGGAC TACAACTGCC ACACACCACC AAAGCTAACT	2400
1629	IGCCARICGC GGGGGGIIII CGIICAGGAC IACAACIGCC ACACACCACC AAAGCIAACI	2400
1630	GACAGGAGAA TCCAGATGGA TGCACAAACA CGCCGCCGCG AACGTCGCGC AGAGAAACAG	2460
1631		
1632	GCTCAATGGA AAGCAGCAAA TCCCCTGTTG GTTGGGGTAA GCGCAAAACC AGTTCCGAAA	2520
1633		
1634	GATTTTTTTA ACTATAAACG CTGATGGAAG CGTTTATGCG GAAGAGGTAA AGCCCTTCCC	2580
1635		
1636	GAGTAACAAA AAAACAACAG CATAAATAAC CCCGCTCTTA CACATTCCAG CCCTGAAAAA	2640
1637		
1638	GGGCATCAAA TTAAACCACA CCTATGGTGT ATGCATTAT TTGCATACAT TCAATCAATT	2700
1639 1640	GTTATCTAAG GAAATACTTA CAT ATG CAA GCT AAA CAT AAA CAA CGT AAA	2750
1641	Met Gln Ala Lys His Lys Gln Arg Lys	2/50
1642	1 5	
1643	-	
1644	CGT CTG AAA TCT AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC AGT	2798
1645	Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser	
1646	10 15 20 25	
1647		
1648	GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC	2846
1649	Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala	
1650	30 35 40	
1651		
1652	TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC	2894
1653 1654	Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn 45 50 55	
1655	43 30 33	
1656	TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT	2942
1657	Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser	
1658	60 65 70	
1659		
1660	AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG	2990
1661	Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser	
1662	75 80 85	
1663	3 MC CMC M3 C CMM C3 C C3 C 3 3 M C3 3 3 3	2020
1664	ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG	3038

Raw Sequence Listing

04/12/93 13:29:28 S4317.raw

1665 1666 1667	Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln 90 95 100 105	
1668 1669	GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA Asp Met Val Val Glu Gly Cys Gly Cys Arg	3088
1670 1671	110 115	
1672	CATAAATATA TATATATA TATATTTTAG AAAAAAGAAA AAAATCTAGA GTCGACCTGC	3148
1673 1674	AGTAATCGTA CAGGGTAGTA CAAATAAAAA AGGCACGTCA GATGACGTGC CTTTTTTCTT	2200
1675	AGIANICGIA CAGGGIAGIA CAANIAAAAA AGGCACGICA GAIGACGIGC CITITITCIT	3208
1676	GTGAGCAGTA AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCTGG	3268
1677 1678	CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA	2220
1679	CGITACCCAA CITAATCGCC TIGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA	3328
1680	AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGCGCCT	3388
1681 1682	GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAT ATGGTGCACT	3448
1683	GRIGOGGIAI IIICICCIIR CGCRICIGIG CGGIRIIICA CACCGCRIRI RIGGIGCACI	3440
1684	CTCAGTACAA TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC	3508
1685 1686	GCTGACGCGC CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC	3560
1687	GCIGACGCGC CCIGACGGGC IIGICIGCIC CCGGCAICCG CIIACAGACA AGCIGIGACC	3568
1688	GTCTCCGGGA GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGA	3623
1689		
1690 1691	(2) INFORMATION FOR SEQ ID NO:14:	
1692	(-,	
1693	(i) SEQUENCE CHARACTERISTICS:	
1694 1695	(A) LENGTH: 115 amino acids (B) TYPE: amino acid	
1696	(D) TOPOLOGY: linear	
1697	, ,	
1698	(ii) MOLECULE TYPE: protein	
1699 1700	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
1701	(XI) DEGORNOE DESCRIPTION. SEQ ID NO.14:	
1702	Met Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys	
1703	1 5 10 15	
1704 1705	Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp	
1706	20 25 30	
1707		
1708	Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys	
1709 1710	35 40 45	
1711	Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val	
1712	50 55 60	
1713		
1714 1715	Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys	
. , . ¬	65 70 75 90	
1715	65 70 75 80	

Raw Sequence Listing

04/12/93 13:29:40 S4317.raw

1717 1718 1719	Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn 85 90 95	
1720 1721 1722	Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys 100 105 110	
1723 1724 1725 1726	Gly Cys Arg 115	
1727 1728	(2) INFORMATION FOR SEQ ID NO:15:	
1729 1730 1731 1732 1733 1734	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
1735 1736 1737 1738	(ii) MOLECULE TYPE: DNA	
1739 1740	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
1741	CATGGGCAGC TGAG	14
1742 1743 1744	(2) INFORMATION FOR SEQ ID NO:16:	
1745 1746 1747 1748 1749	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
1751 1752 1753 1754	(ii) MOLECULE TYPE: DNA	
1755 1756	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
1757 1758	GAGGGTTGTG GGTGTCGCTA GTGAGTCGAC TACAGCAAAT T	41
1759 1760	(2) INFORMATION FOR SEQ ID NO:17:	
1761 1762 1763 1764 1765 1766	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA 	
1768		

Raw Sequence Listing

04/12/93 13:29:47 S4317.raw

1769		
1770		
1771	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
1772		
1773	GGATGTGGGT GCCGCTGACT CTAGAGTCGA CGGAATTC	38
1774	(4)	
1775	(2) INFORMATION FOR SEQ ID NO:18:	
1776		
1777	(i) SEQUENCE CHARACTERISTICS:	
1778 1779	(A) LENGTH: 31 base pairs	
1779	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
1781	(C) SIRANDEDNESS: BINGIE (D) TOPOLOGY: linear	
1782	(D) TOPOLOGI: Tillear	
1783	(ii) MOLECULE TYPE: DNA	
1784	(II) Modecode IIII. DAA	
1785		
1786		
1787	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
1788	(, b-g baboniliation, bag ab notio.	
1789	AATTCACCAT GATTCCTGGT AACCGAATGC T	31
1790		-
1791	(2) INFORMATION FOR SEQ ID NO:19:	
1792		
1793	(i) SEQUENCE CHARACTERISTICS:	
1794	(A) LENGTH: 25 base pairs	
1795	(B) TYPE: nucleic acid	
1796	(C) STRANDEDNESS: single	
1797	(D) TOPOLOGY: linear	
1798		
1799	(ii) MOLECULE TYPE: DNA	
1800		
1801		
1802		
1803	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
1804		
1805	GTGGTACTAA GGACCATTGG CTTAC	25
1806	(0) THEORY TOU TOU TO BE A TO WAR	
1807	(2) INFORMATION FOR SEQ ID NO:20:	
1808	(4) CROWENCE CHARLESTONICS.	
1809 1810	(i) SEQUENCE CHARACTERISTICS:	
1810	(A) LENGTH: 27 base pairs	
1811	(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
1813	(C) STRANDEDNESS: SINGLE (D) TOPOLOGY: linear	
1814	(D) IOLOHOGI: IIHGGI	
1815	(ii) MOLECULE TYPE: DNA	
1816	(II) MODECOME IIIE. DAN	
1817		
1818		
1819	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
1820		

Raw Sequence Listing

04/12/93 13:29:54 S4317.raw

1821 1822	CGACCTGCAG CCATGCATCT GACTGTA	27
1823 1824	(2) INFORMATION FOR SEQ ID NO:21:	
1825	(i) SEQUENCE CHARACTERISTICS:	
1826	(A) LENGTH: 27 base pairs	
1827	(B) TYPE: nucleic acid	
1828	(C) STRANDEDNESS: single	
1829	(D) TOPOLOGY: linear	
1830		
1831	(ii) MOLECULE TYPE: DNA	
1832		
1833		
1834		
1835	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
1836		
1837	TGCCTGCAGT TTAATATTAG TGGCAGC	27
1838	(2) THEORYMETON BOD GEO TO NO 00	
1839 1840	(2) INFORMATION FOR SEQ ID NO:22:	
1841	(i) SEQUENCE CHARACTERISTICS:	
1842	(A) LENGTH: 15 base pairs	
1843	(B) TYPE: nucleic acid	
1844	(C) STRANDEDNESS: single	
1845	(D) TOPOLOGY: linear	
1846	(5) 1010201. 111001	
1847	(ii) MOLECULE TYPE: DNA	
1848	(,	
1849		
1850		
1851	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
1852		
1853	CGACCTGCAG CCACC	15
1854		
1855	(2) INFORMATION FOR SEQ ID NO:23:	
1856		
1857	(i) SEQUENCE CHARACTERISTICS:	
1858	(A) LENGTH: 81 base pairs	
1859	(B) TYPE: nucleic acid	
1860	(C) STRANDEDNESS: single	
1861 1862	(D) TOPOLOGY: linear	
1862	(44) MOLEGILE MUDE. DVX	
1864	(ii) MOLECULE TYPE: DNA	
1865		
1866		
1867	(xi) SEQUENCE DESCRIPTION: SEO ID NO:23:	
1868	,	
1869	TCGACCCACC ATGCCGGGGC TGGGGCGGAG GGCGCAGTGG CTGTGCTGGT GGTGGGGGCT	60
1870		
1871	GTGCTGCAGC TGCTGCGGGC C	81
1872		

Raw Sequence Listing

04/12/93 13:30:00 S4317.raw

1873	(2) INFORMATION FOR SEQ ID NO:24:	
1874	(*) GEOVERNA GUIDI GEORGA	
1875	(i) SEQUENCE CHARACTERISTICS:	
1876	(A) LENGTH: 73 base pairs	
1877	(B) TYPE: nucleic acid	
1878	(C) STRANDEDNESS: single	
1879	(D) TOPOLOGY: linear	
1880	(11)	
1881	(ii) MOLECULE TYPE: DNA	
1882		
1883		
1884		
1885	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
1886		
1887	CGCAGCAGCT GCACAGCAGC CCCCACCACC AGCACAGCCA CTGCGCCCTC CGCCCCAGCC	60
1888		
1889	CCGGCATGGT GGG	73
1890	/A) ====================================	
1891	(2) INFORMATION FOR SEQ ID NO:25:	
1892	///	
1893	(i) SEQUENCE CHARACTERISTICS:	
1894	(A) LENGTH: 11 base pairs	
1895	(B) TYPE: nucleic acid	
1896	(C) STRANDEDNESS: single	
1897	(D) TOPOLOGY: linear	
1898	(11)	
1899	(ii) MOLECULE TYPE: DNA	
1900		
1901	ı	
1902 1903	(
1903	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
1904	TCGACTGGTT T	
1905	ICGACIGGII I	11
1907	(2) INFORMATION FOR SEQ ID NO:26:	
1907	(2) INFORMATION FOR SEQ ID NO:20:	
1909	(i) SEQUENCE CHARACTERISTICS:	
1910	(A) LENGTH: 9 base pairs	
1911	(B) TYPE: nucleic acid	
1912	(C) STRANDEDNESS: single	
1913	(D) TOPOLOGY: linear	
1914	(b) Totologi. Illigat	
1915	(ii) MOLECULE TYPE: DNA	
1916	(11) MONECONE III B. DAN	
1917		
1918		
1919	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
1920	(
1921	CGAAACCAG	9
1922		
1923	(2) INFORMATION FOR SEQ ID NO:27:	
1924	,_,	

Raw Sequence Listing

04/12/93 13:30:07 S4317.raw

1925 1926 1927 1928 1929 1930	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
1931 1932 1933	(ii) MOLECULE TYPE: DNA	
1934 1935	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
1936 1937	TCGACAGGCT CGCCTGCA	18
1938 1939	(2) INFORMATION FOR SEQ ID NO:28:	
1940 1941 1942 1943 1944 1945	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
1946 1947 1948 1949	(ii) MOLECULE TYPE: DNA	
1950 1951	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
1952 1953	GTCCGAGCGG	10
1954		
-	(2) INFORMATION FOR SEQ ID NO:29:	
1955 1956 1957 1958 1959 1960	(2) INFORMATION FOR SEQ ID NO:29: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
1955 1956 1957 1958 1959 1960 1961 1962 1963 1964	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA	29
1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	29
1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29: CAGGTCGACC CACCATGCAC GTGCGCTCA	29

Raw Sequence Listing

04/12/93 13:30:14 S4317.raw

1977 1978 (ii) MOLECULE TYPE: DNA 1979 1980 1981	
1982 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 1983	
1984 TCTGTCGACC TCGGAGGAGC TAGTGGC 1985	27
1986 (2) INFORMATION FOR SEQ ID NO:31: 1987	
1988 (i) SEQUENCE CHARACTERISTICS: 1989 (A) LENGTH: 1794 base pairs	
1990 (B) TYPE: nucleic acid	
1991 (C) STRANDEDNESS: double	
1992 (D) TOPOLOGY: linear	
1993	
1994 (ii) MOLECULE TYPE: DNA	
1995 1996 (vi) ORIGINAL SOURCE:	
1997 (A) ORGANISM: bmp-3	
1998	
1999 (ix) FEATURE:	
2000 (A) NAME/KEY: CDS	
2001 (B) LOCATION: 3211136	
2002	
2003	
2004 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31: 2005	
2005 2006 AGATCTTGAA AACACCCGGG CCACACACGC CGCGACCTAC AGCTCTTTCT CAGCGTTGGA	60
2007	80
	120
2009	•
2010 CCCACCTGTC AGGCTGCGCT GGGTCAGCGC AGCAAGTGGG GCTGGCCGCT ATCTCGCTGC	180
2011	
	240
2013	
	300
2015	350
2016 CGCCGCGCG GTACCTAGCC ATG GCT GGG GCG AGC AGG CTG CTC TTT CTG Met Ala Gly Ala Ser Arg Leu Leu Phe Leu	350
2017 Met Ala Gly Ala Ser Arg Led File Led 2018 1 5 10	
2019	
	398
2021 Trp Leu Gly Cys Phe Cys Val Ser Leu Ala Gln Gly Glu Arg Pro Lys	
2022 15 20 25	
2023	
	446
2025 Pro Pro Phe Pro Glu Leu Arg Lys Ala Val Pro Gly Asp Arg Thr Ala	
2026 30 35 40 2027	
2027 2028 GGT GGT GGC CCG GAC TCC GAG CTG CAG CCG CAA GAC AAG GTC TCT GAA	

Raw Sequence Listing

04/12/93 13:30:21 S4317.raw

2029 2030	Gly	Gly	Gly 45	Pro	Asp	Ser	Glu	Leu 50	Gln	Pro	Gln	Asp	Lys 55	Val	Ser	Glu	
2031																	
2032			CTG														542
2033	His		Leu	Arg	Leu	Tyr	Asp	Arg	Tyr	Ser	Thr	Val	Gln	Ala	Ala	Arg	
2034		60					65					70					
2035																	
2036			GGC														590
2037		Pro	Gly	Ser	Leu		Gly	Gly	Ser	Gln		Trp	Arg	Pro	Arg		
2038	75					80					85					90	
2039																	
2040			GAA														638
2041	Leu	Arg	Glu	GTA		Thr	Val	Arg	Ser		Arg	Ala	Ala	Ala		Glu	
2042					95					100					105		
2043	3 CM	amm	<i>a</i>			~~	ama	m. m	. ma	mm ~		ama					606
2044 2045			GAA														686
2045	Inr	Leu	Glu	_	гув	GIY	Leu	Tyr		Pne	ABN	теп	Inr		Leu	Thr	
2046				110					115					120			
2047	N N C	TO T	GAA	3 3 C	አጥጥ	ጥጥር	TO THE	000	202	CITIC C	m a m	mma	m/cm	a mm	CCA	a a a	734
2049			Glu														/34
2050	пуь	261	125	VOII	110	пец	261	130	1111	пеп	TÄT	FIIIG	135	116	GTĀ	GIU	
2051			143					130					133				
2052	CTT A	GGA	AAC	ΔΤС	AGC	СТС	ΣСΤ	тст	CCA	CTC	ጥርጥ	CCA	CCA	ጥርር	שרכ	СУТ	782
2053			Asn														702
2054		140			561	200	145	Cyb	110	Val	Der	150	GLY	Cyb	Der	1110	
2055																	
2056	CAT	GCT	CAG	AGG	AAA	CAC	ATT	CAG	ATT	GAT	CTT	TCT	GCA	TGG	ACC	CTC	830
2057			Gln														
2058	155					160					165					170	
2059																	
2060	AAA	TTC	AGC	AGA	AAC	CAA	AGT	CAA	CTC	CTT	GGC	CAT	CTG	TCA	GTG	GAT	878
2061	Lys	Phe	Ser	Arg	Asn	Gln	Ser	Gln	Leu	Leu	Gly	His	Leu	Ser	Val	Asp	
2062					175					180	_				185	_	
2063																	
2064	ATG	GCC	AAA	TCT	CAT	CGA	GAT	ATT	ATG	TCC	TGG	CTG	TCT	AAA	GAT	ATC	926
2065	Met	Ala	Lys	Ser	His	Arg	Asp	Ile	Met	Ser	Trp	Leu	Ser	Lys	Asp	Ile	
2066				190					195					200			
2067																	
2068			TTC														974
2069	Thr	Gln	Phe	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Glu	Glu	Phe	Leu	Ile	Gly	
2070			205					210					215				
2071																	
2072			ATT														1022
2073	Phe		Ile	Thr	Ser	Lys		Arg	Gln	Leu	Pro	_	Arg	Arg	Leu	Pro	
2074		220					225					230					
2075							~	a- -									
2076		-	GAG														1070
2077		Pro	Glu	Pro	туr		тел	vaı	TYT	АТА		Asp	АТА	АТА	тте		
2078	235					240					245					250	
2079 2080	G A C	CCX	GAA	y Cum	CTC.	CT X	ጥርን	N.C.C	א נדינדו	CAC	CCA	CNC	CCC	יייגג	ффф	CCC	1118
4000	GAG	CCA	GAA	AG I	GIG	GIA	ICA	AGC	IIM	CAG	GGA	CAC	CGG	WYI	111		1110

Raw Sequence Listing

04/12/93 13:30:27 S4317.raw

2081 2082 2083	Glu Pro Glu Ser Val Val Ser Ser Leu Gln Gly His Arg Asn Phe Pro 255 260 265	
2084	ACT GGA ACT GTT CCC AAA TGGGATAGCC ACATCAGAGC TGCCCTTTCC	1166
2085 2086	Thr Gly Thr Val Pro Lys 270	
2087	2.70	
2088	ATTGAGCGGA GGAAGAAGCG CTCTACTGGG GTCTTGCTGC CTCTGCAGAA CAACGAGCTT	1226
2089		
2090 2091	CCTGGGGCAG AATACCAGTA TAAAAAGGAT GAGGTGTGGG AGGAGAGAAA GCCTTACAAG	1286
2092	ACCCTTCAGG CTCAGGCCCC TGAAAAGAGT AAGAATAAAA AGAAACAGAG AAAGGGGCCT	1346
2093		
2094	CATCGGAAGA GCCAGACGCT CCAATTTGAT GAGCAGACCC TGAAAAAGGC AAGGAGAAAG	1406
2095 2096		1466
2096	CAGTGGATTG AACCTCGGAA TTGCGCCAGG AGATACCTCA AGGTAGACTT TGCAGATATT	1466
2098	GGCTGGAGTG AATGGATTAT CTCCCCCAAG TCCTTTGATG CCTATTATTG CTCTGGAGCA	1526
2099		
2100 2101	TGCCAGTTCC CCATGCCAAA GTCTTTGAAG CCATCAAATC ATGCTACCAT CCAGAGTATA	1586
2101	GTGAGAGCTG TGGGGGTCGT TCCTGGGATT CCTGAGCCTT GCTGTGTACC AGAAAGATG	1646
2103		2010
2104	TCCTCACTCA GTATTTTATT CTTTGATGAA AATAAGAATG TAGTGCTTAA AGTATACCCT	1706
2105	1101E01010 E1010E0EE COCEEEC COCEEEC COCEEEC E1100E0EE E1100E	
2106 2107	AACATGACAG TAGAGTCTTG CGCTTGCAGA TAACCTGGCA AAGAACTCAT TTGAATGCTT	1766
2108	AATTCAATCT CTAGAGTCGA CGGAATTC	1794
2109		
2110	(4)	
2111 2112	(2) INFORMATION FOR SEQ ID NO:32:	
2112	(i) SEQUENCE CHARACTERISTICS:	
2114	(A) LENGTH: 272 amino acids	
2115	(B) TYPE: amino acid	
2116	(D) TOPOLOGY: linear	
2117 2118	(ii) MOLECULE TYPE: protein	
2119	(II) MOLECOLE TIPE: protein	
2120	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
2121		
2122	Met Ala Gly Ala Ser Arg Leu Leu Phe Leu Trp Leu Gly Cys Phe Cys	
2123 2124	1 5 10 15	
2124	Val Ser Leu Ala Gln Gly Glu Arg Pro Lys Pro Pro Phe Pro Glu Leu	
2126	20 25 30	
2127		
2128	Arg Lys Ala Val Pro Gly Asp Arg Thr Ala Gly Gly Pro Asp Ser	
2129 2130	35 40 45	
2131	Glu Leu Gln Pro Gln Asp Lys Val Ser Glu His Met Leu Arg Leu Tyr	
2132	50 55 60	

2184

Raw Sequence Listing

04/12/93 13:30:34 S4317.raw

2133																
2134	Agn	Arg	Tier	Cor	Thr	17 n l	Gln	212	212	2	Th∽	Dro	G1 v	g.~	T 011	C1.,
2135	65	AL 9	1 Y L	261	1111	70	GIII	AIG	ALG	AI 9	75	PIO	GIY	per	пеп	80
2136	0.5					, 0					, ,					00
2137	Glv	Gly	Ser	Gln	Pro	Trn	Ara	Pro	Ara	T.e.ii	T.e.11	Δτα	Glu	Glv	Δan	Thr
2138	,	,			85		9		9	90		••• 9	014	- 1	95	
2139					•					-					,,	
2140	Val	Arg	Ser	Phe	Arg	Ala	Ala	Ala	Ala	Glu	Thr	Len	Glu	Ara	Lvs	Glv
2141		9		100	9				105					110	_,_	0 -7
2142																
2143	Leu	Tvr	Ile	Phe	Agn	Leu	Thr	Ser	T.A11	Thr	Lvs	Ser	Glu	Agn	Tle	Leu
2144		-1-	115					120			_,,	50-	125			
2145																
2146	Ser	Ala	Thr	Leu	Tvr	Phe	Cvs	Ile	Glv	Glu	Leu	Glv	Asn	Ile	Ser	Leu
2147		130			-1-		135					140				
2148																
2149	Ser	Сув	Pro	Val	Ser	Glv	Glv	Cvs	Ser	His	His	λla	Gln	Ara	Lvs	нія
2150	145	- 1.5			501	150	O J	0,0			155		·	9	_, _	160
2151																
2152	Ile	Gln	Ile	Asp	Leu	Ser	Ala	Trp	Thr	Leu	Lvs	Phe	Ser	Ara	Asn	Gln
2153					165					170	-1-			5	175	
2154															_, _	
2155	Ser	Gln	Leu	Leu	Glv	His	Leu	Ser	Val	Asp	Met	Ala	Lvs	Ser	His	Arg
2156				180	4				185				-2	190		3
2157																
2158	Asp	Ile	Met	Ser	Trp	Leu	Ser	Lys	Asp	Ile	Thr	Gln	Phe	Leu	Arq	Lvs
2159	_		195					200					205		3	
2160																
2161	Ala	Lys	Glu	Asn	Glu	Glu	Phe	Leu	Ile	Gly	Phe	Asn	Ile	Thr	Ser	Lvs
2162		210					215			•		220				
2163																
2164	Gly	Arg	Gln	Leu	Pro	Lys	Arq	Arg	Leu	Pro	Phe	Pro	Glu	Pro	Tyr	Ile
2165	225	•				230	•	_			235				•	240
2166																
2167	Leu	Val	Tyr	Ala	Asn	Asp	Ala	Ala	Ile	Ser	Glu	Pro	Glu	Ser	Val	Val
2168			_		245	_				250					255	
2169																
2170	Ser	Ser	Leu	Gln	Gly	His	Arg	Asn	Phe	Pro	Thr	Gly	Thr	Val	Pro	Lys
2171				260	_		_		265			_		270		-
2172																
2173																
2174	(2)	INF	ORMA'	CION	FOR	SEQ	ID 1	10:33	3:							
2175																
2176		(i)	SEC	QUEN	CE CE	HARA	CTER:	CSTIC	CS:							
2177						H: 44				3						
2178						nuc!										
2179			-	-		DEDNI			gle							
2180			(I) T	DPOL	OGY:	line	ear								
2181																
2182		(ii)	MOI	LECUI	LE T	YPE:	DNA									
2183								•								

Raw Sequence Listing

04/12/93 13:30:41 S4317.raw

2105		
2185 2186	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
2187		
2188	ATGTCTCATA ATCGTTCTAA AACTCCAAAA AATCAAGAAG CTCTGCGTAT GGCCAACGTG	60
2189		
2190	GCAGAGAACA GCAGCAGCGA CCAGAGGCAG GCCTGTAAGA AGCACGAGCT GTATGTCAGC	120
2191		
2192	TTCCGAGACC TGGGCTGGCA GGACTGGATC ATCGCGCCTG AAGGCTACGC CGCCTACTAC	180
2193		
2194	TGTGAGGGGG AGTGTGCCTT CCCTCTGAAC TCCTACATGA ACGCCACCAA CCACGCCATC	240
2195 2196	GTGCAGACGC TGGTCCACTT CATCAACCCG GAAACGGTGC CCAAGCCCTG CTGTGCGCCC	200
2190	GIGCAGACGC IGGICCACII CAICAACCCG GAAACGGIGC CCAAGCCCIG CIGIGCGCCC	300
2198	ACGCAGCTCA ATGCCATCTC CGTCCTCTAC TTCGATGACA GCTCCAACGT CATCCTGAAG	360
2199	nounce and an interest of the state of the s	300
2200	AAATACAGAA ACATGGTGGT CCGGGCCTGT GGCTGCCACT AGCTCCTCCG AGAATTCAGA	420
2201		
2202	CCCTTTGGGG CCAAGTTTTT CTGGATCCT	449
2203		
2204	(2) INFORMATION FOR SEQ ID NO:34:	
2205		
2206	(i) SEQUENCE CHARACTERISTICS:	
2207	(A) LENGTH: 18 base pairs	
2208	(B) TYPE: nucleic acid	
2209	(C) STRANDEDNESS: single	
2210	(D) TOPOLOGY: linear	
2211		
2212 2213	(ii) MOLECULE TYPE: DNA	
2214		
2214		
2215	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
2217	(AI) DEGORACE DESCRIPTION. DEG ID NO.34.	
2218	CAAGAAGGAG ATATACAT	18
2219		
2220	(2) INFORMATION FOR SEQ ID NO:35:	
2221		
2222	(i) SEQUENCE CHARACTERISTICS:	
2223	(A) LENGTH: 377 base pairs	
2224	(B) TYPE: nucleic acid	
2225	(C) STRANDEDNESS: single	
2226	(D) TOPOLOGY: linear	
2227		
2228	(ii) MOLECULE TYPE: DNA	
2229		
2230		
2231		
2232	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
2233		-
2234	ATGCGTAAAC AATGGATTGA ACCACGTAAC TGTGCTCGTC GTTATCTGAA AGTAGACTTT	60
2235	GCAGATATTG GCTGGAGTGA ATGGATTATC TCCCCCAAGT CCTTTTGATGC CTATTATTGC	
// sh	- (4) (Δ) (4) (4) (1) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4	120

Raw Sequence Listing

04/12/93 13:30:48 S4317.raw

2237							
2238	TCTGGAGCAT	GCCAGTTCCC	CATGCCAAAG	TCTTTGAAGC	CATCAAATCA	TGCTACCATC	180
2239							
2240	CAGAGTATAG	TGAGAGCTGT	GGGGGTCGTT	CCTGGGATTC	CTGAGCCTTG	CTGTGTACCA	240
2241							
2242	GAAAAGATGT	CCTCACTCAG	TATTTTATTC	TTTGATGAAA	ATAAGAATGT	AGTGCTTAAA	300
2243							
2244	GTATACCCTA	ACATGACAGT	AGAGTCTTGC	GCTTGCAGAT	AACCTGGCAA	AGAACTCATT	360
2245							
2246	TGAATGCTTA	ATTCAAT					377

PAGE:

1

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/864,692A

DATE: 04/12/93 TIME: 13:30:48

S4317

LINE ERROR

ORIGINAL TEXT

Wrong application Serial Number
 Response Exceeds Line Limitations
 Response Exceeds Line Limitations

(A) APPLICATION NUMBER: US 07/864,692 cDNA library #936208

PAGE: 1

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/07/864,692A

DATE: 04/12/93 TIME: 13:30:48

S4317

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA APPLICATION NUMBER FILING DATE

PAGE:

1

LINE ORIGINAL TEXT

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/07/864,692A

CORRECTED TEXT

DATE: 04/12/93 TIME: 13:30:48

S4317